

(FILE 'HOME' ENTERED AT 16:14:42 ON 21 JUN 2004)

FILE 'MEDLINE, BIOSIS, SCISEARCH, BIOTECHDS, CAPLUS' ENTERED AT 16:15:02  
ON 21 JUN 2004

L1 35108 S TYROSINE(W)PHOSPHATASE# OR PTP# OR PTPR#  
L2 2424 S PLOWMAN?/AU  
L3 17 S L1 AND L2  
L4 9 DUP REM L3 (8 DUPLICATES REMOVED)  
L5 0 S BAHIJA?/AU  
L6 81 S PTP5 OR (PTP(W)5) OR PTP05  
L7 78 S L6 AND PY<1998  
L8 49 DUP REM L7 (29 DUPLICATES REMOVED)  
L9 7607 S L1 AND (ADIPOSE OR FAT OR HEMATOPUIETIC OR HAEMATOPUIETIC OR  
L10 1750 S L1(5A) (HEMATOPUIETIC OR HAEMATOPUIETIC OR (T OR B OR NK) (W) (C  
L11 48 S L1(5A) (FAT OR ADIPOSE)  
L12 18 S L11 AND PY<1998  
L13 12 DUP REM L12 (6 DUPLICATES REMOVED)

FILE 'PCTFULL, USPATFULL, EUROPATFULL' ENTERED AT 17:11:43 ON 21 JUN 2004

L14 8955 S TYROSINE(W)PHOSPHATASE# OR PTP#  
L15 16 S L14(5A) (FAT OR ADIPOSE)  
L16 468 S L14/TI,AB  
L17 151 S L16 AND (FAT OR ADIPOSE)  
L18 8 S L17 AND PD<19970611  
L19 948 S L14 AND ADIPOSE  
L20 117 S L14(S)ADIPOSE  
L21 0 S L20 AND PD<19970611  
L22 2 S L20 AND AD<19970611

FILE 'MEDLINE' ENTERED AT 17:24:29 ON 21 JUN 2004

L23 1 S (95 AND 2806 AND 1995)/SO

FILE 'STNGUIDE' ENTERED AT 17:26:04 ON 21 JUN 2004

FILE 'MEDLINE, BIOSIS, SCISEARCH, CANCERLIT, LIFESCI, BIOTECHDS, CAPLUS'  
ENTERED AT 17:26:29 ON 21 JUN 2004

L24 172 S L1(S) (FAT OR ADIPOSE)  
L25 40615 S TYROSINE(W)PHOSPHATASE# OR PTP# OR PTPR#  
L26 115 S L25(S)ADIPOSE  
L27 38 S L26 AND PY<1998  
L28 19 DUP REM L27 (19 DUPLICATES REMOVED)

=>

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:31:57 ; Search time 59 Seconds  
(without alignments)  
2217.280 Million cell updates/sec

Title: US-09-095-478a-6  
Perfect score: 2439  
Sequence: 1 MSAPRYKRGKRGKNDDEEG.....QYQFCYEIVLEVLQNLALY 463

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_2903n04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2439	100.0	463	2	AAW89250
2	2212.5	90.7	426	2	AAW89249
3	2104.5	86.3	405	2	AAW89251
4	1378.5	56.5	420	5	AAE14454
5	1345	55.1	508	7	ADBE08106
6	1309.5	53.7	561	4	ABG06042
7	1306	53.5	398	5	ABG30845
8	1305	53.5	398	5	ADDS9795
9	1306	53.5	409	7	ADBE09123
10	1304.5	53.5	412	6	AAE37996
11	1071	43.9	261	6	AAE37994
12	640	26.2	1267	4	AAAG67637
13	640	26.2	1267	4	AAAG67458
14	639.5	26.2	2466	6	ABU70688
15	639.5	26.2	2466	2	AAW75999
16	639.5	26.2	2466	2	AAW75999
17	639.5	26.2	2466	3	AAI190272
18	639.5	26.2	2466	3	AAI190272
19	566	23.2	122	2	AAW89252
20	501	20.5	913	2	AAW12522
21	501	20.5	913	2	AAW12522
22	501	20.5	913	5	AAW79333
23	501	20.5	913	5	AAW79333
24	496.5	20.4	1948	7	ADD22982
25	496.5	20.4	1949	7	ADD18742

26	496.5	20.4	1949	7	ADDE57121	ADDE57121 Human pro
27	496.5	20.4	1949	7	ADD47019	ADD47019 Human pro
28	496.5	20.4	1949	7	ADD47015	ADD47015 Human pro
29	490.5	20.1	1911	2	AAW71726	AAW71726 Human pro
30	490.5	20.1	1911	2	AAW71725	AAW71725 Human pro
31	490.5	20.1	1911	2	AAW94027	AAW94027 Human pro
32	490.5	20.1	1911	2	AAW94027	AAW94027 Human pro
33	487	20.0	291	4	AAW78282	AAW78282 Human pro
34	487	20.0	1337	2	AAW85203	AAW85203 huDBP-1.
35	484.5	19.9	1175	7	ADDE83529	ADDE83529 Rat prote
36	484.5	19.9	1175	7	ADDE61029	ADDE61029 Rat prote
37	484.5	19.9	1175	7	ADDE61033	ADDE61033 Rat prote
38	483.5	19.8	1439	2	AAW63632	AAW63632 Human rec
39	481.5	19.7	1463	6	ABJ37035	ABJ37035 Human bre
40	481.5	19.7	1463	3	ABJ75519	ABJ75519 Prostate
41	481.5	19.7	1520	5	ABJ05584	ABJ05584 Breast ca
42	480	19.7	1462	4	ABW59384	ABW59384 Human pro
43	479.5	19.7	1462	5	ABW97521	ABW97521 Novel hum
44	479.5	19.7	1440	2	AAW29591	AAW29591 Human pro
45	479.5	19.7	1495	5	ABW57380	ABW57380 Rat mucoc

## ALIGNMENTS

AAW89250	standard; protein; 463 AA.
AAW89250	
AC	AAW89250;
DT	10-MAR-1999 (first entry)
XX	
DB	Mouse PTP05 isoform #1.
XX	
KW	PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;
KW	type I receptor serine/threonine kinase; cancer; leukemia; lymphoma;
KW	neurodegenerative disease; neuronal survival; Alzheimer's disease;
KW	Parkinson's disease; Huntington's disease.
XX	
OS	Mus sp.
XX	
PN	W09849317-A2.
PD	
XX	
PF	05-NOV-1998.
XX	
XX	27-APR-1998; 98WO-US008439.
PR	28-APR-1997; 97US-0044428P.
PR	20-MAY-1997; 97US-0047222P.
PR	11-JUN-1997; 97US-0049477P.
PR	11-JUN-1997; 97US-0049756P.
PR	18-JUN-1997; 97US-0049914P.
PR	23-OCT-1997; 97US-0063595P.
XX	
PA	(SUGEN) SUGEN INC.
XX	
PI	Plowman GD, Clary D, Jallal B, Peles E, Omrust S, Markby D;
PI	Courtneidge SA, App H, Hui TH;
XX	
DR	WPI: 1999-009434/01.
XX	
DR	N-PSDB; AAW81745.
XX	
PT	New nucleic acid encoding specific protein tyrosine phosphatases - useful
PT	for identifying specific modulators for treatment and prevention of
PT	cancer and neurodegenerative disease.
XX	
PS	Claim 2; Page 157-158; 193pp; English.
XX	
CC	The present invention describes isolated, enriched or purified nucleic
CC	acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The
CC	present sequence represents mouse PTP05. The above proteins, other than
CC	ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify

CC substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of Alk-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleotides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the proteins

CC Sequence 463 AA;

Query Match 100.0%; Score 2439; DB 2; Length 463;  
Best Local Similarity 100.0%; Pred. No. 3,6e-225;  
Matches 463; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSPKRYGKGTGRNDDEEGNSGNTLNLSLPSSSQKMTPTPYQNKMLKYEHLIDILM 60  
DB 1 MSSPKRYGKGTGRNDDEEGNSGNTLNLSLPSSSQKMTPTPYQNKMLKYEHLIDILM 60  
QY 61 VPLLIKTITWYVFKLMSKGLIFGNKNSENVKPSHLSFDKYELVPEPLESDDEYTW 120  
DB 61 VPLLIKTITWYVFKLMSKGLIFGNKNSENVKPSHLSFDKYELVPEPLESDDEYTW 120  
QY 121 DVSDBSLRRNNSMDESETAGPSKTVSPVLSGSSRLSKDTETSVSEKELTOLAQIRPLIFN 180  
DB 121 DVSDBSLRRNNSMDESETAGPSKTVSPVLSGSSRLSKDTETSVSEKELTOLAQIRPLIFN 180  
QY 181 SSARSAMRDCLNTLQKKEELDIREFLELEQMTLPDDFNSGNTLQNRDNRRLDILPYDS 240  
DB 181 SSARSAMRDCLNTLQKKEELDIREFLELEQMTLPDDFNSGNTLQNRDNRRLDILPYDS 240  
QY 241 TRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQVLENNCVIAMIITRE 300  
DB 241 TRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQVLENNCVIAMIITRE 300  
QY 301 IECGVTKCYSYMPISLKEPLFEHFSVPLETFHTVQYFTVRVQIVKSTGSCVYKHQ 360  
DB 301 IECGVTKCYSYMPISLKEPLFEHFSVPLETFHTVQYFTVRVQIVKSTGSCVYKHQ 360  
QY 361 FTWPDHGTASADPFKIVRYRKSHITGPILVHCSAGVGRGVICDVVFSALIKRY 420  
DB 361 FTWPDHGTASADPFKIVRYRKSHITGPILVHCSAGVGRGVICDVVFSALIKRY 420  
QY 421 SFDIMNIIVTQMRKQRCGMIOTKEOYQFCYEIVLEVLQNTLLALY 463  
DB 421 SFDIMNIIVTQMRKQRCGMIOTKEOYQFCYEIVLEVLQNTLLALY 463

RESULT 2

AAW89249 standard; protein; 426 AA.

AAW89249;

10-MAR-1999 (first entry)

Mouse PTP05.

PTP04; PTP05; SAD; ALP; ALK-7; protein tyrosine phosphatase;

type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;

neurodegenerative disease; neuronal survival; Alzheimer's disease;

Parkinson's disease; Huntington's disease.

mus sp.

WO9849317-A2.

05-NOV-1998.

27-APR-1998; 98WO-US008439.  
28-APR-1997; 97US-0044428P.  
20-MAY-1997; 97US-0047222P.  
11-JUN-1997; 97US-0049477P.  
11-JUN-1997; 97US-0049756P.  
18-JUN-1997; 97US-0049914P.  
23-OCT-1997; 97US-0063555P.  
(SUGEN) SUGEN INC.  
Plozman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;  
Courtneidge SA, App H, Hui TH;  
WPI; 1999-009434/01.  
N-PQDB; AAW81744.  
New nucleic acid encoding specific protein tyrosine phosphatases - useful for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease.  
Claim 2; Page 155-157; 193pp; English.

The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP05, ALP and ALK-7 proteins. The present sequence represents mouse PTP05. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of Alk-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleotides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the proteins

Sequence 426 AA;

Query Match 90.7%; Score 2212.5; DB 2; Length 426;  
Best Local Similarity 92.0%; Pred. No. 1.9e-203;  
Matches 426; Conservative 0; Mismatches 0; Indels 37; Gaps 1;

QY 1 MSSPKRYGKGTGRNDDEEGNSGNTLNLSLPSSSQKMTPTPYQNKMLKYEHLIDILM 60  
DB 1 MSSPKRYGKGTGRNDDEEGNSGNTLNLSLPSSSQKMTPTPYQNKMLKYEHLIDILM 60  
QY 61 VPLLIKTITWYVFKLMSKGLIFGNKNSENVKPSHLSFDKYELVPEPLESDDEYTW 120  
DB 61 VPLLIKTITWYVFKLMSKGLIFGNKNSENVKPSHLSFDKYELVPEPLESDDEYTW 120  
QY 121 DVSDBSLRRNNSMDESETAGPSKTVSPVLSGSSRLSKDTETSVSEKELTOLAQIRPLIFN 180  
DB 121 DVSDBSLRRNNSMDESETAGPSKTVSPVLSGSSRLSKDTETSVSEKELTOLAQIRPLIFN 180  
QY 181 SSARSAMRDCLNTLQKKEELDIREFLELEQMTLPDDFNSGNTLQNRDNRRLDILPYDS 240  
DB 181 SSARSAMRDCLNTLQKKEELDIREFLELEQMTLPDDFNSGNTLQNRDNRRLDILPYDS 240  
QY 241 TRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQVLENNCVIAMIITRE 300  
DB 241 TRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQVLENNCVIAMIITRE 300  
QY 301 IECGVTKCYSYMPISLKEPLFEHFSVPLETFHTVQYFTVRVQIVKSTGSCVYKHQ 360  
DB 301 IECGVTKCYSYMPISLKEPLFEHFSVPLETFHTVQYFTVRVQIVKSTGSCVYKHQ 360  
QY 361 FTWPDHGTASADPFKIVRYRKSHITGPILVHCSAGVGRGVICDVVFSALIKRY 420  
DB 361 FTWPDHGTASADPFKIVRYRKSHITGPILVHCSAGVGRGVICDVVFSALIKRY 420

QY 421 SEDIMNIVTQMRKORCGMIQTKEOYOTCYEIVLEVLONLALY 463  
 DB 384 SFDIMNIVTQMRKORCGMIQTKEOYOTCYEIVLEVLONLALY 426

RESULT 3  
 AAM89251  
 ID AAM89251 standard; protein; 405 AA.  
 XX  
 AC AAM89251;  
 XX  
 DT 10-MAR-1999 (first entry)  
 DE Mouse PTP05 isoform #2.  
 XX  
 KW PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;  
 KW type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;  
 KW neurodegenerative disease; neuronal survival; Alzheimer's disease;  
 KW Parkinson's disease; Huntington's disease.  
 XX  
 OS Mus sp.  
 XX  
 PN MO849317-A2.  
 XX  
 PD 05-NOV-1998.  
 XX  
 PE 27-APR-1998; 98MO-US008439.  
 XX  
 PR 28-APR-1997; 97US-0044428P.  
 PR 20-MAY-1997; 97US-0047222P.  
 PR 11-JUN-1997; 97US-0049477P.  
 PR 11-JUN-1997; 97US-0049756P.  
 PR 18-JUN-1997; 97US-0049914P.  
 PR 23-OCT-1997; 97US-0063595P.  
 XX  
 PA (SUGEN-) SUGEN INC.  
 XX  
 PI Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;  
 PI Courtenidge SA, App H, Hui TH;  
 XX  
 DR MPI; 1999-009434/01.  
 DR N-PSDB; AAV81746.  
 XX  
 PT New nucleic acid encoding specific protein tyrosine phosphatases - useful  
 PT for identifying specific modulators for treatment and prevention of  
 PT cancer and neurodegenerative disease.  
 XX  
 PS Claim 2; Page 158-160; 193pp; English.  
 XX  
 CC The present invention describes isolated, enriched or purified nucleic  
 CC acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The  
 CC present sequence represents mouse PTP05. The above proteins, other than  
 CC ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify  
 CC substances that modulate their activity (i.e. agonists and antagonists,  
 CC including NBP) in vivo or in vitro. These substances are used to treat or  
 CC prevent diseases associated with abnormal signal transduction pathways  
 CC that involve the proteins, particularly cancer (e.g. leukaemia and  
 CC lymphoma), while modulators of ALK-7 (which is a type I receptor  
 CC serine/threonine kinase) are used to promote neuronal survival,  
 CC particularly for treating Alzheimer's, Parkinson's or Huntington's  
 CC diseases. Nucleic acid fragments of the polynucleotides encoding the  
 CC proteins can be used as probes to identify and clone related sequences;  
 CC to detect protein-encoded RNA; to generate transgenic animals and in gene  
 CC therapy (optionally after mutation). Ab are used to determine the  
 CC proteins  
 XX  
 SQ Sequence 405 AA;

Query Match 86.3%; Score 2104.5; DB 2; Length 405;  
 Best Local Similarity 91.6%; Pred. No. 4.1e-193;  
 Matches 405; Conservative 0; Mismatches 0; Indels 37; Gaps 1;

QY 1 MSSPRVKGKGTGNDDEEGNSGNTLNRSLSSSQKATPTKPVQNKMLKTEHLDILIM 60  
 DB 1 MSSPRVKGKGTGNDDEEGNSGNTLNRSLSSSQKATPTK----- 43  
 QY 61 VPLLKTIYNNFKLMKGLIFGNKNSENVKPSHLSFSDKELVYPPPLSDTDEYV 120  
 DB 44 -----IFGNKNSENVKPSHLSFSDKELVYPPPLSDTDEYV 83  
 QY 121 DVSDRLNRNWSMDSETAGPSKTVPVLSGSSRLSKDTETSSEKELTQLAQIRPLIFN 180  
 DB 84 DVSDRLNRNWSMDSETAGPSKTVPVLSGSSRLSKDTETSSEKELTQLAQIRPLIFN 143  
 QY 181 SSARSAMDCLTLQKKEHLDIIRFLEFQVTLPPDFNSGNTLQNRDKRRFDILPYNS 240  
 DB 144 SSARSAMDCLTLQKKEHLDIIRFLEFQVTLPPDFNSGNTLQNRDKRRFDILPYNS 203  
 QY 241 TRVPLKNDYINASTIRLVNHEEYFYATGQPLPETIEDFMQWLNNKNCVIMATRE 300  
 DB 204 TRVPLKNDYINASTIRLVNHEEYFYATGQPLPETIEDFMQWLNNKNCVIMATRE 263  
 QY 301 IECGVTKCYSYWPISLKEPLEEFHFSVPLETFHVTQYFTVRVQIVKSTGSKQCVKELQ 360  
 DB 264 IECGVTKCYSYWPISLKEPLEEFHFSVPLETFHVTQYFTVRVQIVKSTGSKQCVKELQ 323  
 QY 361 FTKMPDHGTPASADPRIKVVRVRSKSHITGPILVNCSAGVGTGVCIDVPSAIEKRY 420  
 DB 324 FTKMPDHGTPASADPRIKVVRVRSKSHITGPILVNCSAGVGTGVCIDVPSAIEKRY 383  
 QY 421 SFDIMNIVTQMRKORCGMIQTK 442  
 DB 384 SFDIMNIVTQMRKORCGMIQTK 405

RESULT 4  
 AAE14454  
 ID AAE14454 standard; protein; 420 AA.  
 XX  
 AC AAE14454;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Human protein phosphatase-4.  
 XX  
 KW Human; protein phosphatase; PP-4; immune system disorder; AIDS; allergy;  
 KW neurological disorder; developmental disorder; Alzheimer's disease;  
 KW cell proliferative disorder; Huntington's disease; arteriosclerosis;  
 KW renal tubular acidosis; gonadal dysgenesis; cancer; adenocarcinoma;  
 KW leukaemia; transgenic animal; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 183..411  
 FT Region /note="Protein-tyrosine phosphatase"  
 FT Active-site 340..398  
 FT /note="Tyrosine specific protein phosphatase active  
 FT site"  
 FT Region 351..363  
 FT /note="Tyr\_phosphatase"  
 FT Domain 362..379  
 FT /label= Transmembrane\_domain  
 XX  
 PN WO200196546-A2.  
 XX  
 PD 20-DEC-2001.  
 XX  
 PE 14-JUN-2001; 2001WO-US019442.  
 XX  
 PR 16-JUN-2000; 2000US-0212447P.  
 PR 22-JUN-2000; 2000US-0213746P.  
 PR 29-JUN-2000; 2000US-0215210P.  
 PR 06-JUL-2000; 2000US-0216529P.  
 PR 12-JUL-2000; 2000US-0218080P.



21-JUL-2000; 2000US-0220117P.  
 (INCY) INCYTE GENOMICS INC.  
 Au-Yang J, Baughn MR, Ding L, Elliott VS, Gandhi AR, Griffin JA, Hefalla A, Kearney L, Lee BA, Lu Y, Nguyen DB, Patterson C, Rankumar J, Reddy R, Sanjanwala MS, Stewart BA, Tang YT, Thornton M, Tribouley CM, Walla NK, Yang J, Yao MG, Yue H; WPI; 2002-090206/12.  
 N-PSDB; AAD24022.  
 Novel polypeptide, useful for diagnosing, treating or preventing disorders of growth and development, immune system, neurological and cell proliferation diseases, comprises cancer protein phosphatase polypeptides.  
 Claim 1: Page 105-106; 116pp; English.  
 The present sequence is human protein phosphatase (pp)-4, pp polynucleotide and polypeptide are useful in the diagnosis, treatment and prevention of immune system disorders, neurological disorders, developmental disorders and cell proliferative disorders. Examples of immune system disorders include acquired immune deficiency syndrome (AIDS), severe combined immunodeficiency disease (SCID), adult respiratory distress syndrome, allergies, amyloidosis, anaemia, asthma, atherosclerosis, Crohn's disease, atopic dermatitis, diabetes mellitus, emphysema, Goodpasture's syndrome, gout, Graves' disease, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome, rheumatoid arthritis, Sjogren's syndrome, scleroderma, systemic sclerosis, trauma; neurological disorders include Alzheimer's disease, Huntington's disease, dementia, epilepsy, Parkinson's disease, mental retardation and other developmental disorders of central nervous system such as Down's syndrome, cerebral palsy, periodic paralysis, mental disorders including mood, anxiety, and schizophrenia disorders, seasonal affective disorder such as akathisia, amnesia, cataplexy, dyskinesia; developmental disorders include e.g. renal tubular acidosis, Duchenne and Becker muscular dystrophy, gonadal dysgenesis, hypothyroidism; cell proliferative disorders include e.g. actinic keratosis, atherosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, psoriasis and cancer including adenocarcinoma, leukaemia. The polypeptide and polynucleotide are further useful for analysing a proteome of a tissue or a cell type, for screening an agonist/antagonist, a compound that specifically binds to it or its modulator. The polynucleotide is useful for creating knock-in humanised animals (pigs) or transgenic animals (mice or rats) to model human disease, for generating a transcript image of a tissue or cell type, which represents the global pattern of gene expression by a particular tissue or cell type.  
 Sequence 420 AA:  
 Query Match 56.5%; Score 1378.5; DB 5; Length 420;  
 Best Local Similarity 59.2%; Pred. No. 2.7e-123;  
 Matches 274; Conservative 52; Mismatches 92; Indels 45; Gaps 3;  
 1 MSSRRKVRGKGTGRDNDEBEGNSGNILRNLSIPSSQKQPTPKYQNKMLKTEHLDIM 60  
 1 MSSRRDRAEPVNYEGNDEBEGNSGNILRNLSIPSSQKQPTPKYQNKMLKTEHLDIM 60  
 61 VFLLIKITWVFLMKGKLIKGNKNSSEWPKSHLSFQDKVLYLPELSPDQETV 120  
 45 -----FENKNSSEKVKSLNLFPHNDEHVEEBSQSDSMW 93  
 121 DVSDRLRNKNSNDSETAGPSKTVSPVLSGSSRLSKDTEYSSEKLTQLAQIRPLIFN 180  
 84 TARGPFRDRSSDEDAAGSQAISPLLS-----DTRKIVSBEGLDQLAQIRPLIFN 136  
 181 SSASASARDCIANTQK-SELDIIRFPLEEQKTLPPDPSNGTLCQNRKRRRDLIPLPD 239  
 137 FHEOTAIKDCIKTEETAAVDIMQFPALELKNLPESFNSGQPSRREKRRRDLIPLPD 196  
 240 STRVPLGKNKDYINASYIRIVNHEEYFYIATQGPTELTEDFQWMLNNQVMIAMITR 299

197 STRVPLGKSKDYINASYIRIVNHEEYFYIATQGPTELTEDFQWMLNNQVMIAMITR 256  
 300 EIRGVYKCYSPYPISEKLEFEHFSVFLETHVQYFVRVQIVKSGTSGCKHL 359  
 257 EIRGGIICHTHYPISEKLEFEHFSVFLETHVQYFVRVQIVKSGTSGCKHL 316  
 360 QPTKMPDHGTPASADPFKIKVRYRKSHITGPIVHCSAGVGTGFCVDFVFAIEKN 419  
 317 QPTKMPDHGTPASADPFKIKVRYRKSHITGPIVHCSAGVGTGFCVDFVFAIEKN 376  
 420 YSPDINIVYQWKEKRCGMQTEKQYQPCBYLTYLQMLAL 462  
 377 CSFNMIVYQWKEKRCGMQTEKQYQPCBYLTYLQMLAL 419  
 Db 377 CSFNMIVYQWKEKRCGMQTEKQYQPCBYLTYLQMLAL 419  
 RESULT 5  
 ADB08106  
 ID ADB08106 standard; protein; 508 AA.  
 AC ADB08106;  
 DT 29-JUN-2004 (first entry)  
 XX DE Novel protein (useful for identifying genetic disorders) #261.  
 XX KW novel gene; novel protein; tissue marker; molecular weight marker;  
 KW chromosome marker; genetic disorder.  
 OS Undefined.  
 XX MO2003054152-A2.  
 PN MO2003054152-A2.  
 XX 03-JUL-2003.  
 PD 10-DEC-2002; 2002MO-US039555.  
 XX 10-DEC-2001; 2001US-0339739P.  
 PR 11-DEC-2001; 2001US-0339453P.  
 PR 14-MAR-2002; 2002US-0365091P.  
 PR 14-MAR-2002; 2002US-0365384P.  
 PR 12-APR-2002; 2002US-0372381P.  
 PR 12-APR-2002; 2002US-0372615P.  
 PR 22-APR-2002; 2002US-00128558.  
 PR 24-APR-2002; 2002US-0376045P.  
 XX (HYSE-) HYSQ INC.  
 PA Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;  
 PI Ghosh M, Xue AJ, Weinman T, Weng G, Zhou P, Drmanac RT, Wang Z;  
 PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;  
 XX WPI; 2003-569235/53.  
 DR N-PSDB; ADB07195.  
 XX New polynucleotides, useful for expressing recombinant proteins for  
 PT analysis, characterization or therapeutic use, or as markers for tissues  
 PT in which the corresponding protein is preferentially expressed.  
 PS Claim 20; SEQ ID NO 1172; 1177pp; English.  
 XX The invention comprises the amino acid and coding sequences of novel  
 CC proteins. The DNA and protein sequences of the invention are useful as:  
 CC markers for tissues in which the corresponding protein is preferentially  
 CC expressed; as molecular weight markers on gels; as chromosome markers or  
 CC tags; to identify chromosomes or to map related gene positions; and to  
 CC compare with endogenous DNA sequences in patients to identify potential  
 CC genetic disorders. The present amino acid sequence represents a protein  
 CC of the invention.  
 XX Sequence 508 AA;  
 SQ Query Match 55.1%; Score 1345; DB 7; Length 508;

Best Local Similarity 58.5%; Pred. No. 5.9e-126;  
Matches 271; Conservative 52; Mismatches 88; Indels 52; Gaps 5;

QY 3 SPR--KRGKGRNDEBEGNSGLNLRNLSPPSSQKMTFKPKVQNKMLKYEHLIDILM 60  
DB 94 SFRICSVNDYEGNDSAD-----LNFELALPSSQENTPSSKY----- 132  
QY 61 VFLLIKTIWYVFLMKGLIFGNKNNSENVKPSHHLSFSDKYELAYPEPLESDPTDETIV 120  
DB 133 -----FEKNVSEKYLRLRPNHNDYDVEBESGSDPSMW 171  
QY 121 DVSRSLRNKNSNDSETAGPSKTVSPVLSGSSSLSDTETSSEKELTQALQIRPLIFN 180  
DB 172 TARGPFRDRWSSSEDEBAGPSQALSPLS-----DTRKIVSEGLDQALQIRPLIFN 224  
QY 181 SSASAMRDCCLNTLQCK--EELDIIRBFLLEQMTLPDPFNSGNTLONRDKRKYDILPYD 239  
DB 225 FHEGTALKDCLKLEKTAAYDLMQEFWALEKMLPSEFYSGNOPSRREKRRIDILPYD 284  
QY 240 STRVPLGKNDYINASYIRIYNHEEYFYATQGPLBETIEDFQWVLENNCVIAMIIR 239  
DB 285 STRVPLGSKDYINASYIRIYNHCEYFYATQGPLSTIDDFQWVLENNSVIAMIIR 344  
QY 300 EIBGVKIKVSYMPISLKEPLEFHFVLETHVNTQYFTVRVQIYKSGTGSQCKHL 359  
DB 345 EMBGGIITKCYHWFISLKEPLELHGFVLENYQIIQYFIIRMFQVVEKSTGTSHSVQOL 404  
QY 360 QFTKMPDHGTASADPFITKTVYVRKSHITGPIVHCSAGVSTGVYICVDVVFSALEKN 419  
DB 405 QFTKMPDHGTASADPFITKTVYVRKSHITGPIVHCSAGVSTGVYICVDVVFSALEKN 464  
QY 420 YSPDINMIVTQMKORCGMLOTKBOYQFCYEIVLEVLONLAL 462  
DB 465 CSFNMIDIVAQMRBQSGWQTKBOYHFCYDVLVLRKLLTL 507

RESULT 6  
ABG06042  
ID ABG06042 standard; protein; 561 AA.  
XX  
AC ABG06042;  
XX  
DT 13-FEB-2002 (first entry)  
XX  
DE Novel human diagnostic protein #6033.  
XX  
KM Human; chromosome mapping; gene mapping; gene therapy; forensic;  
XX food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN MO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PE 30-MAR-2001; 2001WO-US008631.  
XX  
PR 31-MAR-2000; 2000US-00540217.  
XX 23-AUG-2000; 2000US-00649167.  
XX (HYSB-) HYSBQ INC.  
XX  
PI Dmanac RT, Liu C, Tang YT;  
XX  
DR MPI: 2001-639362/73.  
XX N-PSDB; AAS70229.  
XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
XX diagnostics, forensics, gene mapping, identification of mutations  
XX responsible for genetic disorders or other traits and to assess  
XX biodiversity.  
PS Claim 20; SEQ ID NO 36401; 103BP; English.

XX  
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
CC amino acid sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 561 AA;  
XX  
Query Match 53.7%; Score 1309.5; DB 4; Length 561;  
Best Local Similarity 57.3%; Pred. No. 1.8e-116;  
Matches 266; Conservative 59; Mismatches 102; Indels 37; Gaps 7;  
QY 15 NDEBEGNSGLNLRNLS-----PSSQKMTFKPKVQNKMLKYEHLIDILMVELLI----- 65  
DB 118 SODNDEPGSCAVRASCFLMEPYSGR-----VABQGHASILLPSIAIPCCI 164  
QY 66 ----KTIWY--VFPLMKGLIFGNKNNSENVKPSHHLSFSDKYELAYPEPLESDPTDETIV 119  
DB 165 TSNKTKQMLKATITMILHDS--VFENKNSSEKYLRLNRPNDYDVEBESGSDPSMW 223  
QY 120 WDVSRLRNKNSNDSETAGPSKTVSPVLSGSSSLSDTETSSEKELTQALQIRPLIF 179  
DB 224 TARGPFRDRWSSSEDEBAGPSQALSPLS-----DTRKIVSEGLDQALQIRPLIF 276  
QY 180 SSASAMRDCCLNTLQCK--EELDIIRBFLLEQMTLPDPFNSGNTLONRDKRKYDILPY 238  
DB 277 NFHEGTALKDCLKLEKTAAYDLMQEFWALEKMLPSEFYSGNOPSRREKRRIDILPY 336  
QY 239 DSTRVPLGKNDYINASYIRIYNHEEYFYATQGPLBETIEDFQWVLENNCVIAMIIR 298  
DB 337 DSTRVPLGSKDYINASYIRIYNHCEYFYATQGPLSTIDDFQWVLENNSVIAMIIR 396  
QY 299 REIECGVTKCYSYMPISLKEPLEFHFVLETHVNTQYFTVRVQIYKSGTGSQCKVH 358  
DB 397 REMEGGIITKCYHWFISLKEPLELHGFVLENYQIIQYFIIRMFQVVEKSTGTSHSVQOL 456  
QY 359 LOFTKMPDHGTASADPFITKTVYVRKSHITGPIVHCSAGVSTGVYICVDVVFSALEK 418  
DB 457 LOFTKMPDHGTASADPFITKTVYVRKSHITGPIVHCSAGVSTGVYICVDVVFSALEK 516  
QY 419 NYSFDINMIVTQMKORCGMLOTKBOYQFCYEIVLEVLONLAL 462  
DB 517 DCSFNMIDIVAQMRBQSGWQTKBOYHFCYDVLVLRKLLTL 560

RESULT 7  
ABG30845  
ID ABG30845 standard; protein; 398 AA.  
XX  
AC ABG30845;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human tyrosine phosphatase protein #1.  
XX  
KM Human; tyrosine phosphatase; obesity; diabetes; Parkinson's disease;

KM central nervous system disorder; CNS; cardiovascular disorder; stroke;  
 KM chronic obstructive pulmonary disease; cancer; multiple sclerosis;  
 KM Alzheimer's disease; Huntington's disease; congestive heart failure;  
 KM myocardial infarction; chromosome 10.

OS Homo sapiens.

XX MO200242435-A2.

PD 30-MAY-2002.

XX 27-NOV-2001; 2001WO-EP013794.

XX 27-NOV-2000; 2000US-0252912P.

XX (FARB) BAYER AG.

XX Znu Z;

XX MPI, 2002-575236/61.

XX N-PSDB; ABR89178.

PT New human tyrosine phosphatase polypeptide, the regulation of which is  
 PT useful for treating obesity, diabetes, cardiovascular or central nervous  
 PT system disorder, chronic obstructive pulmonary disease and cancer.

XX Claim 25; Fig 2; 145pp; English.

XX The present invention relates to a new human tyrosine phosphatase  
 CC polypeptide. The invention is useful for the preparation of a medicament  
 CC for modulating the activity of human tyrosine phosphatase in a disease  
 CC such as obesity, diabetes, a central nervous system (CNS) disorder,  
 CC chronic obstructive pulmonary disease, cardiovascular disorder or cancer.  
 CC The invention is useful for treating a human tyrosine phosphatase  
 CC dysfunction related disease, preferably the above mentioned diseases. The  
 CC invention is useful for treating the above mentioned disorders, where the  
 CC CNS disorder is selected from Parkinson's disease, multiple sclerosis,  
 CC stroke, Alzheimer's disease, and Huntington's disease, and the  
 CC cardiovascular disorder is selected from congestive heart failure and  
 CC myocardial infarction. The molecules of the invention are useful in  
 CC diagnostic assays for detecting diseases and abnormalities or  
 CC susceptibility to disease and abnormalities related to the presence of  
 CC mutations in the polynucleotide coding the polypeptide of the invention.  
 CC The present amino acid sequence represents the human tyrosine phosphatase  
 CC protein #1 of the invention. This sequence is encoded by the human  
 CC tyrosine phosphatase gene located on chromosome 10  
 CC  
 XX Sequence 398 AA:

Query Match 53.5%; Score 1306; DB 5; Length 398;

Best Local Similarity 65.8%; Pred. No. 2,3e-116; Indels 8; Gaps 2;

Matches 252; Conservative 48; Mismatches 75; Indels 8; Gaps 2;

QY 81 IFGNQNSVAVKPSHLSFSDKYLVPPELESDPTDVTVDVSRSLRNRMNSDSETAG 140  
 DB 22 VFEKQVSEKVKSLKRFPHNDVDFEFSQSDSMVTAGPFRDMSSEDERAG 81  
 QY 141 PSKTVSVGLGSSRLKQDTSTVSEKELTOLAQIRPLFNSSARSARDCLATLQKK-EE 199  
 DB 82 PSQALSPILS-----DTRKIVSEGLDOLAQIRPLFNFHQVQAIKDCIKLLEETAA 134  
 QY 200 LIDIRBELLEQWTLPPDFNSGNTLQNRDKNRYRDIPLYSTVPYKGNQVYNASTIR 259  
 DB 135 YDLMQEMALEKRLPGEFYSGNOPSRKRRRDILPYDSTVPLQSKSDYINASTIR 194  
 QY 260 VNHBEVFYATQGLPEETEDFQWVLENNCNVMIITEIBGVKCYSTYPSLKEP 319  
 DB 195 VNCEBEFYATQGLPLSTIDDFQWVLENNCNVMIITEBEGGIIKCHYPISLKEP 254  
 QY 320 LEPHBEVFLETHVQVTVRVQVYKSKTSQCKHLOFRKPHGHPASADSFIRY 379  
 DB 255 LELKHEVFLENTYQVTVRVQVYKSKTSQCKHLOFRKPHGHPASADSFIRY 314

QY 380 VRVRSKSHITGPIVHCASGVGTGVCIDVVFSAILEKNSPDIMATVYQNRKRCMT 439  
 DB 315 IRYARSSEHLGPPVWVCSASIGRTGVFLCVDFVFCALVDCSPNMDIVAKMSEGRSMV 374  
 QY 440 QTEQYQPCYEIVLEVLQNTLAL 462  
 DB 375 QTEQYHFCYDYLVEVLRLTL 397

RESULT 8

ADD89795

ID ADD89795 standard; protein; 398 AA.

AC ADD89795;

DT 29-JUN-2004 (first entry)

XX Human DKFZP566K0524 protein SEQ ID NO:10.

XX cancer associated phosphatase; enzyme; human; cancer; tumour; cytosolic;  
 XX immunosuppressive; antidiabetic; neuroprotective; antirheumatic;  
 XX antiarthritic; antiproliferative; antidiabetic; antirheumatic;  
 XX vulvar; gynaecological; antidiabetic; antiproliferative disease;  
 KM autoimmune disease; diabetes mellitus; multiple sclerosis;  
 KM rheumatoid arthritis; psoriasis; atherosclerosis; inflammation; scarring;  
 KM endometriosis; angiogenesis.

OS Homo sapiens.

XX MO2003083102-A2.

XX 09-OCT-2003.

XX 19-MAR-2003; 2003WO-CA000393.

XX 28-MAR-2002; 2002US-0368859P.

XX (KINE-) KINETER PHARM INC.

XX Delaney AD;

XX MPI, 2003-902934/82.

XX N-PSDB; ADD89794.

PT New nucleic acids encoding cancer associated phosphatases, useful as  
 PT targets for screening pharmaceutical agents that inhibit the growth of  
 PT tumor cells, or for diagnosing and treating cancer, inflammation or  
 PT autoimmune disease.

XX Claim 1, SEQ ID NO 10; 63pp; English.

XX The present invention describes an isolated cancer associated phosphatase  
 CC nucleic acid. Also described: (1) a method of screening for biologically  
 CC active agents that modulate a cancer associated phosphatase function; (2)  
 CC a method for the diagnosis of cancer; (3) a method for inhibiting the  
 CC growth of a cancer cell; (4) methods of screening for targets of a cancer  
 CC associated phosphatase, where the targets are associated with signal  
 CC transduction in cancer cells; (5) a compound (C) for the treatment of a  
 CC tumour; (6) a composition for the treatment of a tumour comprising a  
 CC pharmaceutical carrier and (C); (7) methods for treating a tumour; and  
 CC (8) a method for visualising a tumour in a patient. A cancer associated  
 CC phosphatase of the present invention has cytosolic, immunosuppressive,  
 CC antidiabetic, neuroprotective, antirheumatic, antiarthritic,  
 CC antiproliferative, antidiabetic, antirheumatic, antiproliferative,  
 CC gynaecological and antidiabetic activities. The cancer associated  
 CC phosphatases and nucleic acids encoding the proteins are useful for  
 CC visualising tumours in patients or diagnosing and treating cancer, e.g.  
 CC pancreas, lung, ovarian, liver or colon cancer. The polypeptides and  
 CC nucleic acids may also be used for treating hyperproliferative diseases,  
 CC such as autoimmune disease, diabetes mellitus, multiple sclerosis,  
 CC rheumatoid arthritis, psoriasis, atherosclerosis, inflammation, scarring,  
 CC endometriosis or angiogenesis, determining the effectiveness of drugs,  
 CC determining patient prognosis, or as targets for screening pharmaceutical

CC agents that inhibit the growth or metastasis of tumour cells. The present  
 CC sequence represents the human cancer associated phosphatase  
 CC DKFZP566K0524, which is used in the exemplification of the present  
 CC invention.

XX Sequence 398 AA:

Query Match 53.5%; Score 1306; DB 7; Length 398;  
 Best Local Similarity 65.8%; Pred. No. 2.3e-116;  
 Matches 252; Conservative 48; Mismatches 75; Indels 8; Gaps 2;

QY 1 FGKNGNSENVKPSHLSFSDKTELVYEPLESDTDETVNDVSDSLRNKNSMDSSTAG 140  
 DB 22 VFENKVSSEKVKLSLRNPNNDYEDVFEPSSESGSDPSMTARAGPFRDRMSSEDEAAG 81  
 QY 141 PSKTVSPVLSGSSRLSKDTETSVSEKELTQLAQIRPLIFNSARSARMDCLNTLQCK-EE 199  
 DB 82 PSQALSPILS-----DTRKIVSEGEJDLQAIIRPLIFNHEGTAIDCLKILEKTA 134  
 QY 200 LDIIFEFLEBOMTLPPDPSNGTLONRDKNRYRDLIPYDSTRVPLGKNKDYINASYIRI 259  
 DB 135 YDIMQEFMALBKMLPGSEFSGNQPSNRKRYRDLIPYDSTRVPLGKSKDYINASYIRI 194  
 QY 260 VNHSEEFYIATOGPLPETIEDFMQVLENNQNVAMITREIEGCVIKCSYMTISLKEP 319  
 DB 195 VNGGEFYTATOGPLSTIDPFQWVLENNSVIAMITREMEGGLIKCYHYMPISLKEP 254  
 QY 320 LFEHFSVPLETFHVQYFTVAVPQIVKSTGSKQCVKHLQFTKMPDHGTPASADPFIKY 379  
 DB 255 LELKHFVPLFENYQILQYFIRMFQVAKSTGTSHSVQLOFTKMPDHGTPASADPFIKY 314  
 QY 380 VRYRKSHITGPIPLVHCSAGVGTGVFCVNVVFSALIEKNVSPDINNIYTORKORCGMI 439  
 DB 315 IRYARKSHLTGPMVHCSAGIGRTGVFLCVDFVFCALVKDSCFNIMDIVAQREQRSGMV 374  
 QY 440 QTEQYQFCYEIVLEVLQNLAL 462  
 DB 375 QTEQYHFCYDIVLEVLARKLTL 397

RESULT 9  
 ADE09123  
 ID ADE09123 standard; protein; 409 AA.

XX ADE09123;  
 AC  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Novel protein-related contig polypeptide sequence #189.  
 XX  
 KM novel gene; novel protein; tissue marker; molecular weight marker;  
 XX chromosome marker; genetic disorder; contig.  
 OS  
 XX Unidentified.

PN W0203054152-A2.

PD 03-JUL-2003.

PF 10-DEC-2002; 2002W0-US039555.

XX  
 PR 10-DEC-2001; 2001US-0339739P.  
 PR 11-DEC-2001; 2001US-0339453P.  
 PR 14-MAR-2002; 2002US-0365091P.  
 PR 14-MAR-2002; 2002US-0365384P.  
 PR 12-APR-2002; 2002US-0372381P.  
 PR 12-APR-2002; 2002US-0372615P.  
 PR 12-APR-2002; 2002US-00128558.  
 PR 24-APR-2002; 2002US-0376045P.

XX (HYSB-) HYSBQ INC.

PA Tang YT, Aundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;  
 PI

PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;  
 PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;  
 DR WPI, 2003-569235/53.

PT New polynucleotides, useful for expressing recombinant proteins for  
 PT analysis, characterization or therapeutic use, or as markers for tissues  
 PT in which the corresponding protein is preferentially expressed.

PS Disclosure; SEQ ID NO 2667; 1177bp; English.

XX The invention comprises the amino acid and coding sequences of novel  
 CC proteins. The DNA and protein sequences of the invention are useful as:  
 CC markers for tissues in which the corresponding protein is preferentially  
 CC expressed; as molecular weight markers on gels; as chromosome markers or  
 CC tags; to identify chromosomes or to map related gene positions; and to  
 CC compare with endogenous DNA sequences in patients to identify potential  
 CC genetic disorders. The present amino acid sequence was used in the  
 CC exemplification of the invention.

XX Sequence 409 AA:

Query Match 53.5%; Score 1306; DB 7; Length 409;  
 Best Local Similarity 65.8%; Pred. No. 2.4e-116;  
 Matches 252; Conservative 48; Mismatches 75; Indels 8; Gaps 2;

QY 81 IFGKNGNSENVKPSHLSFSDKTELVYEPLESDTDETVNDVSDSLRNKNSMDSSTAG 140  
 DB 33 VFENKVSSEKVKLSLRNPNNDYEDVFEPSSESGSDPSMTARAGPFRDRMSSEDEAAG 92  
 QY 141 PSKTVSPVLSGSSRLSKDTETSVSEKELTQLAQIRPLIFNSARSARMDCLNTLQCK-EE 199  
 DB 93 PSQALSPILS-----DTRKIVSEGEJDLQAIIRPLIFNHEGTAIDCLKILEKTA 145  
 QY 200 LDIIFEFLEBOMTLPPDPSNGTLONRDKNRYRDLIPYDSTRVPLGKNKDYINASYIRI 259  
 DB 146 YDIMQEFMALBKMLPGSEFSGNQPSNRKRYRDLIPYDSTRVPLGKSKDYINASYIRI 205  
 QY 260 VNHSEEFYIATOGPLPETIEDFMQVLENNQNVAMITREIEGCVIKCSYMTISLKEP 319  
 DB 206 VNGGEFYTATOGPLSTIDPFQWVLENNSVIAMITREMEGGLIKCYHYMPISLKEP 265  
 QY 320 LFEHFSVPLETFHVQYFTVAVPQIVKSTGSKQCVKHLQFTKMPDHGTPASADPFIKY 379  
 DB 266 LELKHFVPLFENYQILQYFIRMFQVAKSTGTSHSVQLOFTKMPDHGTPASADPFIKY 325  
 QY 380 VRYRKSHITGPIPLVHCSAGVGTGVFCVNVVFSALIEKNVSPDINNIYTORKORCGMI 439  
 DB 326 IRYARKSHLTGPMVHCSAGIGRTGVFLCVDFVFCALVKDSCFNIMDIVAQREQRSGMV 385  
 QY 440 QTEQYQFCYEIVLEVLQNLAL 462  
 DB 386 QTEQYHFCYDIVLEVLARKLTL 408

RESULT 10

AAE37996  
 ID AAE37996 standard; protein; 412 AA.

AC AAE37996;  
 XX

DT 06-NOV-2003 (first entry)  
 XX

DB Human kinase and phosphatase (KPP-41) protein.

XX Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis;  
 XX atherosclerosis; cirrhosis; haemoglobinuria; polycythemia vera; cancer;  
 XX psoriasis; chromocytopenia; developmental disorder; Reiter's syndrome;  
 KM renal tubular acidosis; anemia; mental retardation; Alzheimer's disease;  
 KM neurological disorder; Parkinson's disease; epilepsy; glomerulonephritis;  
 KM autoimmune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome;  
 KM acquired immune deficiency syndrome; immunosuppressive; Crohn's disease;  
 KM noctropic; transgenic; dermatitis; multiple sclerosis; diabetes mellitus;

KW allergy; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome;  
 KW osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological;  
 KW gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.  
 OS Homo sapiens.  
 XX WO2003050084-A2.  
 XX  
 XX 19-JUN-2003.  
 XX  
 XX 06-DEC-2002; 2002WO-US039126.  
 XX  
 XX 07-DEC-2001; 2001US-0340235P.  
 XX 19-DEC-2001; 2001US-0343007P.  
 XX 21-DEC-2001; 2001US-0343546P.  
 XX 04-FEB-2002; 2002US-0354388P.  
 XX 15-FEB-2002; 2002US-0357675P.  
 XX  
 XX (INCY-) INCYTE GENOMICS INC.  
 XX  
 XX Kable AE, Chien D, Wilson AD, Swarnakar A, Gorvad AE;  
 PI Hafalia AD, Emerling BM, Ramkumar J, Jin P, Griffin JA, Margulis JP;  
 PI Baughn MR, Chawla NK, Lehr-Mason PM, Khare R, Lee S, Hawkins PR;  
 PI Becha SD, Lee SY, Sprague WW, Zebardjadian Y;  
 DR WPI; 2003-532894/50.  
 DR N-PSDB; AAD57368.  
 XX  
 XX New human kinases and phosphatases and polynucleotides, useful for  
 PT diagnosing, treating or preventing autoimmune or inflammatory disorders  
 PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,  
 PT cancer or hepatitis.  
 XX  
 XX Claim 1; Page 243-244; 282pp; English.  
 XX  
 XX The invention relates to an isolated polypeptide, which is a human kinase  
 CC and phosphatase (KPP). KPP agonists and antagonists are useful for  
 CC diagnosing, treating or preventing disorders associated with aberrant  
 CC expression of KPP, particularly cell proliferative disorders (e.g.  
 CC arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal  
 CC nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary  
 CC thrombocytopenia or cancer), developmental disorders (eg. renal tubular  
 CC acidosis, anemia or mental retardation), neurological disorders (e.g.  
 CC Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune/  
 CC inflammatory disorders (e.g. AIDS, acquired immune deficiency syndrome,  
 CC allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's  
 CC disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome,  
 CC gout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome,  
 CC multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's  
 CC syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,  
 CC bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP  
 CC is useful in assessing the effects of exogenous compounds on the  
 CC expression of nucleic acids and kinases and phosphatases. KPP gene is  
 CC useful in gene therapy and for creating transgenic animals to model human  
 CC disease. The present sequence is human KPP protein  
 XX  
 XX Sequence 412 AA:  
 SQ  
 Query Match 53.5%; Score 1304.5; DB 6; Length 412;  
 Best Local Similarity 58.6%; Pseq. No. 3.3e-116;  
 Matches 260; Conservative 50; Mismatches 89; Indels 45; Gaps 3;  
 Oy 1 MSSPKVAGTGTGRDDEEGNSGNLINSIPSSSQKTPPKYQNKMKYEEHDLIIM 60  
 Db 1 MSSPDEFAEPVNDDEGNSDEADINFRITLPSSSQETPPSKV----- 44  
 Oy 61 VELLIKITVNVFLKMGKLIIFGKKNKSNENYKPSHLSFSDKVELVYPEPLESTDETVM 120  
 Db 45 -----FENKNSSEKVKLSLRPNHNDYVDVEPSESSESSDSSKM 83  
 Oy 121 DVSRLSLRNKNSMDSRTAGRSKTVSPYLSSGSLSLKDTTSVSEKELLTOLAQIRPIFN 180  
 Db 84 TARGPFRDRWSSDEEAGPSALSPLS-----DTRKIYSEGLDOLAQIRPIFN 136

Oy 181 SSARSARDCCLNTLOKK-BELDITREPLELEQMTLPDDFNSGNTLQNRDRIRDLIPYD 239  
 Db 137 FHEQTALINDCLILEETAAVDIMQEFMALEKNTLPBEPFSGNQPSNRKRRYDILIPYD 196  
 Oy 240 STRVPLGKNQVYNASYRIYNHEEFYATQGPLETIEDFPQWVLNNCVIAMITR 229  
 Db 197 STRVPLGKSDYINASTIRIVNCGEEFYATQGPPLSTIDDPQWVLNNSVIAIMTR 256  
 Oy 300 EIEGVIKCYSPYPSLSEPLEPEBPSVPLEFHTVQYFTVRVFOIVKXSTGSKQCKEL 359  
 Db 257 EIEGIIKCYHWPISIKKLEKHEFVLENTQILOYFIIRHQVYKSTGSHSKOL 316  
 Oy 360 QFTKWPBHGTPASADPFIKYRVYRSKHTGPLLHNSAGVGRTPICVDVPSALEKN 419  
 Db 317 QFTKWPBHGTPASADPFIKYRVYRSKHTGPLLHNSAGVGRTPICVDVPSALEKN 376  
 Oy 420 YSPDINIVTQMRKRCGMIOQKE 443  
 Db 377 CSFIMDIVAQMRBQSGMWQTK 400

## RESULT 11

ID AAE37994 standard; protein; 261 AA.

XX AAE37994:

DT 06-NOV-2003 (first entry)

XX Human kinase and phosphatase (KPP-39) protein.

KW Human; kinases; phosphatase; KPP; cell proliferative disorder; hepatitis;  
 KW atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer;  
 KW psoriasis; thrombocytopenia; developmental disorder; Reiter's syndrome;  
 KW renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease;  
 KW neurological disorder; Parkinson's disease; epilepsy; glomerulonephritis;  
 KW autoimmune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome;  
 KW acquired immune deficiency syndrome; immunosuppressive; Crohn's disease;  
 KW nocturnal; transgenic; dermatitis; multiple sclerosis; diabetes mellitus;  
 KW allergy; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome;  
 KW osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological;  
 KW gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.

XX Homo sapiens.

XX WO2003050084-A2.

XX 19-JUN-2003.

XX 06-DEC-2002; 2002WO-US039126.

XX 07-DEC-2001; 2001US-0340235P.

XX 19-DEC-2001; 2001US-0343007P.

XX 21-DEC-2001; 2001US-0343546P.

XX 04-FEB-2002; 2002US-0354388P.

XX 15-FEB-2002; 2002US-0357675P.

XX (INCY-) INCYTE GENOMICS INC.

XX Kable AE, Chien D, Wilson AD, Swarnakar A, Gorvad AE;  
 PI Hafalia AD, Emerling BM, Ramkumar J, Jin P, Griffin JA, Margulis JP;  
 PI Baughn MR, Chawla NK, Lehr-Mason PM, Khare R, Lee S, Hawkins PR;  
 PI Becha SD, Lee SY, Sprague WW, Zebardjadian Y;  
 DR WPI; 2003-532894/50.  
 DR N-PSDB; AAD57368.

PT New human kinases and phosphatases and polynucleotides, useful for  
 PT diagnosing, treating or preventing autoimmune or inflammatory disorders  
 PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,  
 PT cancer or hepatitis.  
 XX

PS Claim 1; Page 242; 282PP; English.

XX The invention relates to an isolated polypeptide, which is a human kinase  
CC and phosphatase (KPP). KPP agonists and antagonists are useful for  
CC diagnosing, treating or preventing disorders associated with aberrant  
CC expression of KPP, particularly cell proliferative disorders (e.g.  
CC arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal  
CC nocturnal haemoglobinuria, polycythemia vera, psoriasis, primary  
CC thrombocytopenia or cancer), developmental disorders (eg. renal tubular  
CC acidosis, anaemia or mental retardation), neurological disorders (e.g.  
CC Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune/  
CC inflammatory disorders (e.g. AIDS; acquired immune deficiency syndrome,  
CC allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's  
CC disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome,  
CC gout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome,  
CC multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's  
CC syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,  
CC bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP  
CC is useful in assessing the effects of exogenous compounds on the  
CC expression of nucleic acids and kinases and phosphatases. The KPP  
CC is useful in gene therapy and for creating transgenic animals to model human  
CC disease. The present sequence is human KPP protein

XX Sequence 261 AA;

Query Match 43.9%; Score 1071; DB 6; Length 261;  
Best Local Similarity 75.8%; Pred. No. 4.5e-94;  
Matches 197; Conservative 28; Mismatches 35; Indels 0; Gaps 0;

QY 203 IREPLEEQMTLPDDFNSGNTLQNRDKRYADILPYDSTRVPLGKNDYINASYIRLVNH 262  
DB 1 MQEPMALDKNLPEPFNSGNSPNSREKRYRDLIPYSTVPLGSKNDYINASTIRLVNC 60  
QY 263 EEEFFYATGCPLEPTTEDFQNTLENNCNVIANITREICGVIKCYSPISLKEPLEF 322  
DB 61 GEEFFYATGCPLEPTTEDFQNTLENNCNVIANITREICGVIKCYSPISLKEPLEF 120  
QY 323 EHEFFVLETFVDTQYFVAVFQIVKSTGSKQCVKSHQFTKWPDHGPASADSPFXVRY 382  
DB 121 KHPFVLENNQILOFTIIRMFQVVKSTGTSVKQLOFTKWPDHGPASADSPFXIKIRY 180  
QY 383 VRKSHITGPELLVHCSAGVGTGTFICVDVYFSALEKNYSPDINNTVTKMKQKQCMIOYK 442  
DB 181 ARKSHLTGPMVHCSAGIGRTGVFLCVDVYFCAIVKCSFNIMDIVAQKQSGSMVQTK 240  
QY 443 EKOYFCFEIVLVQNTLAL 462  
DB 241 EOHFPCYDIVLEVRKULTL 260

RESULT 12  
AA67637  
ID AA67637 standard; protein; 1267 AA.

AC AA67637;

DT 26-NOV-2001 (first entry)

XX Amino acid sequence of a human protein.

XX Human; protein kinase; protein phosphatase; signal transduction.

XX Homo sapiens.

XX MO200109316-A1.

XX 08-FEB-2001.

XX 28-JUL-2000; 2000WO-JP005061.

XX 23-JUL-1999; 99JP-00248036.

XX 18-OCT-1999; 99US-0159590P.

XX 11-JAN-2000; 2000JP-00118776.

PR 17-FEB-2000; 2000US-0183322P.  
PR 02-MAY-2000; 2000JP-00183767.  
PR 09-JUN-2000; 2000JP-00241899.

PA (HELI-) HELIX RES INSR.

XX Oca T, Isogai T, Nishikawa T, Hayaishi K, Saito K, Yamamoto J;  
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;  
XX Senoo C, Nezu J;

DR WPI; 2001-570286/64.

PT New genes encoding proteins with protein kinase/protein phosphatase  
PT activity, useful in the diagnosis and treatment of diseases.

XX Example 4; Page 206-215; 233pp; Japanese.

XX The specification describes human protein kinase/protein phosphatases. It  
CC is expected that the protein kinase/protein phosphatase gene participates  
CC in signal transduction in cells. The protein kinase/protein phosphatase  
CC polypeptides and polynucleotides are useful for developing diagnostics  
CC and treatment agents for human and animal diseases. The protein  
CC kinase/protein phosphatase polypeptides are useful as target molecules in  
CC designing novel drugs. The protein kinase/protein phosphatase  
CC polynucleotides are useful as a source of probes and primers, which may  
CC be used to isolate homologous sequences. The present sequence represents  
CC a human protein, which is used in the course of the invention

SQ Sequence 1267 AA;

Query Match 26.2%; Score 640; DB 4; Length 1267;  
Best Local Similarity 38.0%; Pred. No. 1.5e-51;  
Matches 137; Conservative 62; Mismatches 128; Indels 34; Gaps 6;

QY 108 PEPLSDTDETVWDVSDRSILRRNMSMSETAGPSTVSPVLSGSSRLSKDSTSVSEKE 167  
DB 922 PQEKTTDDEITWG-NDLEPIERTNHESD-----KD-HSFLTND 960  
QY 168 LTVLAQIRPLINSSARSMDCINTLO-----KKEEDITREPLEEQMTLPDDFNSG 221  
DB 961 LAVLPVAVKLPFGKTYTGANLKSIVIRLVARSGIPSEKLENTQELKPLDQCL-----G 1014  
QY 222 NTLQNRDKRYADILPYDSTRVPLGKNDYINASYIRLVNHEEYFIATGCPLEPTIED 281  
DB 1015 QTKENRRKRYKNTLIPYATIRVPLGDEBGYINASPKIKIVGKEEYFIATGCPLEPTI 1074  
QY 282 FQOMVLENNCNVIANITREIECGVTKCYSPISL-KEPLSEHFSVLETFHVDTQYFV 340  
DB 1075 FQOMVLEKSTVIANMTQVEGEEKI KQRYWNIIGKTTMVSNRLALVFMQQLKGFV 1134  
QY 341 RVFOIVKSTGSKQCVKSHQFTKWPDHGPASADSPFXIKVRYVRKSHITGPELLVHCSAGV 400  
DB 1135 RANLTEDITREVRISHNLFTAMPDHDTPSQPDLLPFIISYRHHISGPIITHOSAGI 1194  
QY 401 GRTGVFICVDVYFSALEKNYSPDINNTVTKMKQKQCMIOYKQFCYBIYLVQNTL 460  
DB 1195 GRSGLTICIDVYLGILSQDLDPDISDILVRCYALQHGKGVQTEQDTLFCQVILVYLVRLQ 1254  
QY 461 A 461  
DB 1255 A 1255

RESULT 13  
AA67458  
ID AA67458 standard; protein; 1267 AA.

AC AA67458;

DT 26-NOV-2001 (first entry)

XX Amino acid sequence of a human polypeptide.

KW Human; protein kinase; protein phosphatase; signal transduction;  
 KM intracellular signalling pathway.  
 XX Homo sapiens.  
 XX MO200109345-A1.  
 XX 08-FEB-2001.  
 XX 28-JUL-2000; 2000WO-JP005060.  
 XX 29-JUL-1999; 99JP-00248036.  
 XX 18-OCT-1999; 99US-0159590P.  
 XX 11-JAN-2000; 2000JP-00118776.  
 XX 17-FEB-2000; 2000US-0183322P.  
 XX 02-MAY-2000; 2000JP-00183767.  
 XX (HELI-) HELIX RES INST.  
 XX Ota T, Isegai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J,  
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Furuhashi S,  
 PI Senoo C, Nezu J;  
 XX MPI; 2001-564736/63.  
 XX  
 XX New genes encoding protein kinase and protein phosphatase, useful for  
 PT identifying modulators which can be used to treat human or animal  
 PT disorders associated with the expression or function of these enzymes.  
 XX  
 XX Example 4: Page 305-315; 336pp; Japanese.  
 XX  
 XX The specification describes human protein kinase/protein phosphatases.  
 CC The polypeptides are expected to participate in signal transduction in  
 CC cells. The kinase phosphatases are connected with intracellular  
 CC signalling pathways. Antisense oligonucleotides and compounds identified  
 CC by screening (agonists or antagonists) can be used to treat human or  
 CC animal disorders associated with the expression or function of the  
 CC protein. In addition, the polypeptides may be used as target molecules  
 CC for drug development. The present sequence represents a polypeptide, used  
 CC in the course of the invention  
 CC  
 XX  
 XX Sequence 1267 AA;  
 SQ  
 Query Match 26.2%; Score 640; DB 4; Length 1267;  
 Best Local Similarity 38.0%; Pred. No. 1.5e-51;  
 Matches 137; Conservative 62; Mismatches 128; Indels 34; Gaps 6;  
 QY 108 PEPESDTEWVSDRSILRNKNSMDETAGPSKTVSPVLSSSSRLSKDTEVSSEK 167  
 DB 922 POKKTDDEDTWG-NDELPIERTNHEDS-----KD-HSFLTND 960  
 QY 168 LTQALQIRPLIFNSASASAMDCINTLQ-----KKEELDIRREPLEQWTLRDDNSG 221  
 DB 961 LAVIPYAVVLSGKYTGANKLSVRLVRAVSAGSPSEKELNQLKXLDOLI-----G 1014  
 QY 222 NTLQNRNRRVRLPLPDSTFVPLGKNDYINASYIRIWNHEEYFIYANOGEPLPTIED 281  
 DB 1015 QTKENRRNRKRYKTLIPDATTVPPLGDESGYINASFIRIPVGEKFFVYIACGPIPTVGD 1074  
 QY 282 FMOVLENNQVIMITREIEGVIKCVSWPISL-KEPLEFHFSLERFHTOYFTV 340  
 DB 1075 FMOVHWEKSYIVIAMTQVEVGEKIKCORVFNILGKTWVSNRLALVHMQQLKFPV 1134  
 QY 341 RVFOIVKSTGSKOCVKRLQFTKMPDHGTSPASADFFIKVYVYKSHITGELLVHSGAGV 400  
 DB 1135 RAMTLEDIQTRVESHISHTNFTAMPDHTPQPDLLFTFISYMHIRSGPIITHCSAGI 1194  
 QY 401 GRTGVFCVDVYFSAIEKNYSFDIMNYVTQMKROCMQKQKQCYCEHIVLEVYQNL 460  
 DB 1195 GRSGLICIDVVLGISQDLDFDISLVRCRLQHRGVOTEDQYIFCYVILVLRLO 1254  
 QY 461 A 461

DB 1255 A 1255  
 RESULT 14  
 ABU70688  
 ID ABU70688 standard; protein; 766 AA.  
 XX  
 XX AC ABU70688;  
 XX DT 10-JUN-2003 (first entry)  
 XX  
 XX DE Human adipocyte Selected Interacting domain, SID, #319.  
 XX  
 XX KW Human; prey; adipocyte; SID; selected interacting domain; anorectic;  
 KW antididiabetic; protein-protein interaction; diabetes;  
 KW yeast 2-hybrid assay; metabolic disorder; obesity.  
 XX  
 XX OS Homo sapiens.  
 XX  
 XX PN MO200286122-A2.  
 XX PD 31-OCT-2002.  
 XX  
 XX PF 14-MAR-2002; 2002WO-EP003768.  
 XX  
 XX PR 14-MAR-2001; 2001US-0275734P.  
 XX  
 XX PA (HYBR-) HYBRIGENICS.  
 XX  
 XX PI Legrain P, Davlet L;  
 XX  
 XX DR MPI; 2003-103412/09.  
 XX DR N-PSDB; ACAS7232.  
 XX  
 XX PT New complex between two interacting proteins in adipocyte cells, useful  
 PT for identifying selected interacting domains that modulate protein  
 PT interactions, or for preventing or treating metabolic disorders such as  
 PT obesity or diabetes.  
 XX  
 XX  
 XX PS Claim 6; Page 208-209; 382pp; English.  
 XX  
 XX The invention relates to a complex between two interacting proteins in  
 CC adipocyte cells, given in the specification. The proteins are identified  
 CC by selecting a bait protein from a known adipocyte marker and then  
 CC performing a yeast 2-hybrid selection to isolate prey proteins encoded by  
 CC members of an adipocyte cDNA library. The proteins are designated SID  
 CC (RTM) (selected interacting domain) proteins. Also included are a  
 CC polynucleotide encoding a polypeptide in the adipocyte cells, a  
 CC recombinant host cell expressing at least one of the interacting  
 CC polypeptides of the complex, selecting a modulating compound in adipocyte  
 CC cells, a SID (RTM) polypeptide comprising any of the 738 amino acid  
 CC sequences given in the specification (including its fragment or variant),  
 CC a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences  
 CC given in the specification (including its fragment or variant), a vector  
 CC comprising the SID (RTM) polynucleotide, a recombinant host cell  
 CC comprising the vector, a protein chip comprising the polypeptides and a  
 CC record comprising all or part of the data, listed in the specification.  
 CC The complex, polypeptides, polynucleotides and compounds are useful for  
 CC preventing or treating metabolic disorders such as obesity or diabetes.  
 CC The polynucleotides are useful as probes or primers. The complex is  
 CC particularly useful for identifying selected interacting domains (SID  
 CC (RTM)) for screening drugs that modulate the protein interaction, thus  
 CC exhibiting the therapeutic effect. The present sequence represents a SID  
 CC (prey) protein of the invention  
 CC  
 XX  
 XX Sequence 766 AA;  
 SQ  
 Query Match 26.2%; Score 639.5; DB 6; Length 766;  
 Best Local Similarity 37.8%; Pred. No. 7.3e-52;  
 Matches 137; Conservative 62; Mismatches 128; Indels 35; Gaps 6;  
 QY 108 PEPESDTEWVSDRSILRNKNSMDETAGPSKTVSPVLSSSSRLSKDTEVSSEK 167  
 DB 922 POKKTDDEDTWG-NDELPIERTNHEDS-----KD-HSFLTND 960

Db 420 PQEKKTDDEITWG-NDLEPIERTNHEDSD-----KD-HSFLTND 458  
 Qy 168 LTQIAQIRPLIFNSSASAMRDCLNTLQ-----KKELDIIRFLEBQMTLPDDFNS 220  
 Db 459 LAVLPVVKVLPSSKKTGANLKSIVRLRGLLDQGISPEKLENTLQELKPLDQCLT----- 512  
 Qy 221 GNTLQNRDKNRYRDLIPYDSTRVPLGKNDYINASYIRIVNHEEYFYATOGPLPETIE 280  
 Db 513 GGTENRRKRRKRYKTLIPDATRVPLGDEGGYINASFYIKI PVKKEEFYIACGGPLPTVG 572  
 Qy 281 DFMQWLENNCNVYIAMITREIECGVYIKCYSTWPISL-KEPLEFHPVSFLETFHTVQYFT 339  
 Db 573 DFMQWLENNCNVYIAMITREIECGVYIKCYSTWPISL-KEPLEFHPVSFLETFHTVQYFT 339  
 Qy 340 VRVFOIVKSGTSGSCVYKLOFTKWPDPGTSPASADFFIKYRYVRKSHITGPLVHCSAG 399  
 Db 633 VRVATLIEDIQTRVAVHSHLNTAMPDHPDTPSQDDLTFTISYMRHRSGLPIITHCSAG 692  
 Qy 400 VGRGVVFCVDVVFSAIEKNYSFDIMNTVTOMRKQRCGMQTKBOYQFCYEVILEVLONL 459  
 Db 693 IGRSGTLICIDVYLGILSQDLDPDISLVRQCRMLQRHGMVQTEDQYIFCYQVILVLTIRL 752  
 Qy 460 IA 461  
 Db 753 QA 754

RESULT 15  
 AAR71498

ID AAR71498 standard; protein; 2466 AA.

XX AAR71498;

AC 25-MAR-2003 (revised)  
 DT 05-OCT-1995 (first entry)

XX Human protein tyrosine phosphatase PTPPL.

XX Protein tyrosine phosphatase; PTPPL.

XX Homo sapiens.

XX Key Location/Qualifiers  
 470, 505

XX Region /label=Leucine zipper motif  
 570, 585

XX FT Region /note="homology to the band 4.1 superfamily"

XX W09506735-A2.

XX PD 09-MAR-1995.

XX PF 01-SEP-1994; 94MO-US009943.

XX PR 01-SEP-1993; 93US-00115573.

XX PA (LUDWIG-) LUDWIG INST CANCER RES.

XX PI Gomez LJ, Saras J, Claesson-Welsh L, Heldin C;

XX DR MPI; 1995-115450/15.

XX DR N-PSDB; AA085924.

XX PT New protein tyrosine phosphatase(s), PTPPL and GLM-2 - used to develop  
 prod. for use in detection, diagnosis, screening assays or therapy.

XX PS Claim 9; Page 56-68; 92pp; English.

XX A cDNA library was prepared from human glioma cell line U-343 Mga 31L or  
 CC AG1518 human fibroblast cDNA library was also screened. The complete ORF  
 CC of PTPPL was derived from six overlapping cDNA clones and is given in  
 CC the antisense oligo was AA085928. Three clones defined novel PTP  
 CC sequences. Two of these were named PTPPL and GLM-2. The U-343 Mga 31L

CC cDNA library was screened with labeled probes corresp. to PTPPL. The  
 CC AG1518 human fibroblast cDNA library was also screened. The complete ORF  
 CC of PTPPL was derived from six overlapping cDNA clones and is given in  
 CC AA085924. (Updated on 25-MAR-2003 to correct PN field.)  
 CC  
 XX  
 SQ Sequence 2466 AA;

Query Match 26.2%; Score 639.5; D2 2; Length 2466;  
 Best local similarity 37.8%; Pred. No. 4.6e-51;  
 Matches 137; Conservative 62; Mismatches 126; Indels 35; Gaps 6;

Qy 108 PEPESDTDETVDVSDNSLRNRNMSDSTAGPSKTVSPVLSGSSRLSKDTETYSKKE 167  
 Db 2120 PQEKKTDDEITWG-NDLEPIERTNHEDSD-----KD-HSFLTND 2158  
 Qy 168 LTQIAQIRPLIFNSSASAMRDCLNTLQ-----KKELDIIRFLEBQMTLPDDFNS 220  
 Db 2159 LAVLPVVKVLPSSKKTGANLKSIVRLRGLLDQGISPEKLENTLQELKPLDQCLT----- 2212  
 Qy 221 GNTLQNRDKNRYRDLIPYDSTRVPLGKNDYINASYIRIVNHEEYFYATOGPLPETIE 280  
 Db 2213 GGTENRRKRRKRYKTLIPDATRVPLGDEGGYINASFYIKI PVKKEEFYIACGGPLPTVG 2272  
 Qy 281 DFMQWLENNCNVYIAMITREIECGVYIKCYSTWPISL-KEPLEFHPVSFLETFHTVQYFT 339  
 Db 2273 DFMQWLENNCNVYIAMITREIECGVYIKCYSTWPISL-KEPLEFHPVSFLETFHTVQYFT 339  
 Qy 340 VRVFOIVKSGTSGSCVYKLOFTKWPDPGTSPASADFFIKYRYVRKSHITGPLVHCSAG 399  
 Db 2333 VRVATLIEDIQTRVAVHSHLNTAMPDHPDTPSQDDLTFTISYMRHRSGLPIITHCSAG 2392  
 Qy 400 VGRGVVFCVDVVFSAIEKNYSFDIMNTVTOMRKQRCGMQTKBOYQFCYEVILEVLONL 459  
 Db 2393 IGRSGTLICIDVYLGILSQDLDPDISLVRQCRMLQRHGMVQTEDQYIFCYQVILVLTIRL 2452  
 Qy 460 IA 461  
 Db 2453 QA 2454

Search completed: June 16, 2004, 19:38:35  
 Job time : 62 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:37:28 ; Search time 23 Seconds  
(without alignments)  
1039,253 Million cell updates/sec

Title: US-09-095-478A-6

Perfect score: 2439  
Sequence: 1 MSSPRKVRKGTGRNDEEG.....QYQPCYEIVLEVIQNLITALLY 463

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A COMB pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B COMB pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A COMB pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B COMB pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PTUS COMB pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfile1 pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	639.5	26.2	2465 2 US-08-596-291-3	Sequence 3, Appl1
2	639.5	26.2	2465 3 US-09-100-804-3	Sequence 3, Appl1
3	639.5	26.2	2466 3 US-09-080-855-12	Sequence 12, Appl1
4	639.5	26.2	2466 4 US-09-566-076-12	Sequence 12, Appl1
5	639.5	26.2	2466 5 PCT-US94-09943-2	Sequence 2, Appl1
6	639.5	26.2	2485 3 US-09-290-640-46	Sequence 46, Appl1
7	639.5	26.2	2485 4 US-09-665-615B-46	Sequence 46, Appl1
8	501	20.5	913 4 US-09-848-294-2	Sequence 2, Appl1
9	494	20.3	244 4 US-09-848-294-7	Sequence 7, Appl1
10	490.5	20.1	1911 1 US-08-348-006B-5	Sequence 5, Appl1
11	490.5	20.1	1911 2 US-08-800-825A-5	Sequence 5, Appl1
12	490.5	20.1	1911 3 US-09-158-657-5	Sequence 5, Appl1
13	490.5	20.1	1911 5 PCT-US94-10166-5	Sequence 5, Appl1
14	489	20.0	231 2 US-08-446-345-37	Sequence 37, Appl1
15	487	20.0	242 2 US-08-685-992-21	Sequence 21, Appl1
16	487	20.0	242 3 US-09-144-925-21	Sequence 21, Appl1
17	487	20.0	1337 3 US-08-854-585-2	Sequence 2, Appl1
18	487	20.0	1337 4 US-09-447-533-2	Sequence 2, Appl1
19	487	20.0	1337 5 PCT-US95-05512-2	Sequence 2, Appl1
20	483.5	19.8	1439 2 US-08-449-644-2	Sequence 2, Appl1
21	483.5	19.8	1439 3 US-08-087-244A-2	Sequence 2, Appl1
22	480.5	19.7	278 1 US-08-201-697-16	Sequence 16, Appl1
23	477.5	19.6	1457 2 US-08-652-971-3	Sequence 3, Appl1
24	477.5	19.6	1457 3 US-08-449-644-1	Sequence 1, Appl1
25	477.5	19.6	1457 2 US-08-087-244A-1	Sequence 1, Appl1
26	477.5	19.6	1457 2 US-08-991-258A-3	Sequence 3, Appl1
27	477.5	19.6	1457 2 US-08-769-399-3	Sequence 3, Appl1

28	477.5	19.6	1457 3 US-08-991-953A-3	Sequence 3, Appl1
29	476	19.5	1501 2 US-08-447-644-3	Sequence 3, Appl1
30	476	19.5	1501 2 US-08-716-679-3	Sequence 3, Appl1
31	471.5	19.3	1174 2 US-08-446-345-36	Sequence 36, Appl1
32	468	19.2	1452 2 US-08-449-644-8	Sequence 8, Appl1
33	468	19.2	1452 2 US-08-087-244A-8	Sequence 8, Appl1
34	467	19.1	2314 4 US-09-816-703A-2	Sequence 2, Appl1
35	466.5	19.1	232 2 US-08-446-345-38	Sequence 38, Appl1
36	466	19.1	1452 2 US-08-552-971-4	Sequence 4, Appl1
37	466	19.1	1452 2 US-08-991-258A-4	Sequence 4, Appl1
38	466	19.1	1452 2 US-08-769-399-4	Sequence 4, Appl1
39	466	19.1	1452 3 US-08-991-953A-4	Sequence 4, Appl1
40	462.5	19.0	245 2 US-08-685-992-26	Sequence 26, Appl1
41	462.5	19.0	245 2 US-09-144-925-26	Sequence 26, Appl1
42	462	18.9	1188 1 US-08-201-697-4	Sequence 4, Appl1
43	459.5	18.8	2308 1 US-08-015-973-1	Sequence 1, Appl1
44	459.5	18.8	2308 2 US-08-448-164-1	Sequence 1, Appl1
45	459.5	18.8	2308 3 US-08-081-929-2	Sequence 2, Appl1

## ALIGNMENTS

RESULT 1  
US-08-596-291-3  
Sequence 3, Application US/08596291  
Patent No. 5821075  
GENERAL INFORMATION:  
APPLICANT: GONZALEZ, LEONEL JORGE  
APPLICANT: SARAS, JAN  
APPLICANT: CLAESSON-WELSH, LENA  
TITLE OF INVENTION: HELDIN, CARL-HENRIK  
TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL  
TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
STREET: 600 ATLANTIC AVENUE  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/596,291  
FILING DATE: 09-AUG-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/115,573  
FILING DATE: 01-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: GATES, EDWARD R.  
REGISTRATION NUMBER: 31,616  
REFERENCE/DOCKET NUMBER: 10461/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/720-3500  
TELEFAX: 617/720-2441  
TELEX: 92-1742 EZEKIL  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2465 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-596-291-3  
Query Match 26.2%; Score 639.5; DB 2; Length 2465;  
Best Local Similarity 37.8%; Pred. No. 1.6e-53;

Matches 137; Conservative 62; Mismatches 128; Indels 35; Gaps 6;

QY 108 PEPLESDTETWVDVSDRSLENNRNSMDETSKTVSPVLSGSSSLKOTETSSEKE 167  
 DB 2119 POKKTDDEITWG-NDLEPIERTNHEDS-----KD-HSFLTNDE 2157  
 QY 168 LTQLAQIRPLFNSSASAMDCANTLQ-----KKEELDIREFLEQLPDDFNS 220  
 DB 2158 LAVLPVVKVLPBSKRTGANKSVIRLRGLDQIPSKELNQLKPLDQCL----- 2211  
 QY 221 GNTLQNRDKRRYDILPYDSTVPLGKNKDYINASYIRLVNHEEYFYIATGCLPETIE 280  
 DB 2212 GGTENRRKRRYKILPYDARVPLGEGGYNASPKIPGKEEFYIACQGLPFTWG 2271  
 QY 281 DFMQWLENNKNCVIAITREIECGVICKSYMPISL-KEPLEFHEHVSLETHVQYPT 339  
 DB 2272 DFMQWLENNKNCVIAITREIECGVICKSYMPISL-KEPLEFHEHVSLETHVQYPT 2331  
 QY 340 VRVFOIVKSKTGSCQVCKLOFTKMPDHGTPASADPFIKYRVYRKSHITGPLLHCSAG 399  
 DB 2332 VRAMTLEDIQTRVNRHSHLFTAMPDHDTPSPDDLLTFISYMRHHRSGPIITHCSAG 2391  
 QY 400 VERTGVFCVDVVFSAIEKNYSFDINIVTQKROKCGMIQYKQYQFCYETIVLYQNL 459  
 DB 2392 IGRSGTLICIDVTLGILISQDLDFDISDLVRGRLQHRGMVQTEDOYIFCYQVILVLTSL 2451  
 QY 460 LA 461  
 DB 2452 QA 2453

RESULT 2  
 US-09-100-804-3  
 ; Sequence 3, Application US/09100804  
 ; Patent No. 6086472  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GONZALEZ, LEONEL JORGE  
 ; APPLICANT: SARAS, JAN  
 ; APPLICANT: CLAUSSON-WEISS, LENA  
 ; APPLICANT: HELDIN, CARL-HENRIK  
 ; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL  
 ; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN  
 ; NUMBER OF SEQUENCES: 34  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
 ; STREET: 600 ATLANTIC AVENUE  
 ; CITY: BOSTON  
 ; STATE: MASSACHUSETTS  
 ; COUNTRY: USA  
 ; ZIP: 02210  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.25  
 ; CURRENT APPLICATION NUMBER: US/09/100.804  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/596,291  
 ; FILING DATE: 09-AUG-1996  
 ; APPLICATION NUMBER: US 08/115,573  
 ; FILING DATE: 01-SEP-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US94/09943  
 ; FILING DATE: 01-SEP-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: GATES, EDWARD R.  
 ; REGISTRATION NUMBER: 31,616  
 ; REFERENCE/DOCKET NUMBER: L0461/7003  
 ; TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-720-3500  
 TELEFAX: 617-720-2441  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2465 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-100-804-3

Query Match 26.2%; Score 639.5; DB 3; Length 2465;  
 Best Local Similarity 37.8%; Pred. No. 1.6e-53;  
 Matches 137; Conservative 62; Mismatches 128; Indels 35; Gaps 6;

QY 108 PEPLESDTETWVDVSDRSLENNRNSMDETSKTVSPVLSGSSSLKOTETSSEKE 167  
 DB 2119 POKKTDDEITWG-NDLEPIERTNHEDS-----KD-HSFLTNDE 2157  
 QY 168 LTQLAQIRPLFNSSASAMDCANTLQ-----KKEELDIREFLEQLPDDFNS 220  
 DB 2158 LAVLPVVKVLPBSKRTGANKSVIRLRGLDQIPSKELNQLKPLDQCL----- 2211  
 QY 221 GNTLQNRDKRRYDILPYDSTVPLGKNKDYINASYIRLVNHEEYFYIATGCLPETIE 280  
 DB 2212 GGTENRRKRRYKILPYDARVPLGEGGYNASPKIPGKEEFYIACQGLPFTWG 2271  
 QY 281 DFMQWLENNKNCVIAITREIECGVICKSYMPISL-KEPLEFHEHVSLETHVQYPT 339  
 DB 2272 DFMQWLENNKNCVIAITREIECGVICKSYMPISL-KEPLEFHEHVSLETHVQYPT 2331  
 QY 340 VRVFOIVKSKTGSCQVCKLOFTKMPDHGTPASADPFIKYRVYRKSHITGPLLHCSAG 399  
 DB 2332 VRAMTLEDIQTRVNRHSHLFTAMPDHDTPSPDDLLTFISYMRHHRSGPIITHCSAG 2391  
 QY 400 VERTGVFCVDVVFSAIEKNYSFDINIVTQKROKCGMIQYKQYQFCYETIVLYQNL 459  
 DB 2392 IGRSGTLICIDVTLGILISQDLDFDISDLVRGRLQHRGMVQTEDOYIFCYQVILVLTSL 2451  
 QY 460 LA 461  
 DB 2452 QA 2453

RESULT 3  
 US-09-080-855-12  
 ; Sequence 12, Application US/09080855A  
 ; Patent No. 6083721  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Saraz, Jan  
 ; APPLICANT: Franz, Petra  
 ; APPLICANT: Aspernstrm, Pontus  
 ; APPLICANT: Hellman, Ulf  
 ; APPLICANT: Gonzalez, Leonel Jorge  
 ; APPLICANT: Heldin, Carl-Henrik  
 ; TITLE OF INVENTION: PARC, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PP2L  
 ; FILER REFERENCE: L0461/7030  
 ; CURRENT APPLICATION NUMBER: US/09/080.855A  
 ; CURRENT FILING DATE: 1998-05-18  
 ; EARLIER APPLICATION NUMBER: 08/805,583  
 ; EARLIER FILING DATE: 1997-02-25  
 ; NUMBER OF SEQ ID NOS: 39  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 12  
 ; LENGTH: 2465  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-080-855-12

Query Match 26.2%; Score 639.5; DB 3; Length 2465;  
 Best Local Similarity 37.8%; Pred. No. 1.6e-53;  
 Matches 137; Conservative 62; Mismatches 128; Indels 35; Gaps 6;

QY 108 PEPLESDTDETVWVDSRLRNKNSMDETAAPSKTVSPVLSGSSRLSDTETSSEKE 167  
DB 2120 POKKTDDEITWG-NDELPIERTNHEDSD-----KD-HSFLTND 2158  
QY 168 LTOAQRPLIFNSSASAMDCINTLO-----KKEELDIREFLEBOMTLPPDFNS 220  
DB 2159 LAVPVAVKLPESGKYTGANKSVIRVRLGDLGIPSKLEENQELKPLDQCL----- 2212  
QY 221 GNTLQNDKRRYRDLIPYDSTRVPLGKNDYINASYIRIYNHEEYFIATQCPLETTIE 280  
DB 2213 GQTEENRRKRRYRDLIPYDSTRVPLGEGYINASFYIKIPVGEHEVYIATQCPLETTVG 2272  
QY 281 DEMQVLENNQNVAMITREIEGCVIKCYSTYPISTL-KEPLERHSPVLETFHVTQYFT 339  
DB 2273 DEMQVLENNQNVAMITREIEGCVIKCYSTYPISTL-KEPLERHSPVLETFHVTQYFT 2332  
QY 340 VRVFOIVKSGTGKSCCVHLOFTKMPDHGTASADPFIKYRVYRKSHITGPLLHCSAG 399  
DB 2333 VRAMTLEDIQTRVNHISHLNFMTAPDHDTSPDPDLTFLISYRHHRSQPIITHCSAG 2392  
QY 400 VGRGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCMIQTEQOYOCYEIVLEVONL 459  
DB 2393 IGRSGTLICIDVVLGLISQDLFDISDLVRCMRQHRGMQTEBOYIFCYVILVYLTRL 2452  
QY 460 LA 461  
DB 2453 QA 2454

RESULT 4  
US-09-566-076-12  
Sequence 12, Application US/09566076  
Patent No. 645775

GENERAL INFORMATION:  
APPLICANT: Saras, Jan  
APPLICANT: Franz, Petrus  
APPLICANT: Aspenstrm, Pontus  
APPLICANT: Hellman, Ulf  
APPLICANT: Gomez, Leonel Jorge  
APPLICANT: Heidig, Carl-Henrik  
TITLE OF INVENTION: PARAG A STRAISE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPPL  
FILE REFERENCE: L0461/7030  
CURRENT APPLICATION NUMBER: US/09/566,076  
CURRENT FILING DATE:  
EARLIER APPLICATION NUMBER: 09/080,855  
EARLIER FILING DATE: 1998-05-18  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 12  
LENGTH: 2466  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-566-076-12

Query Match 26.2%; Score 639.5; DB 4; Length 2466;  
Best Local Similarity 37.8%; Pred. No. 1.6e-53;  
Matches 137; Conservative 62; Mismatches 128; Indels 35; Gaps 6;

QY 108 PEPLESDTDETVWVDSRLRNKNSMDETAAPSKTVSPVLSGSSRLSDTETSSEKE 167  
DB 2120 POKKTDDEITWG-NDELPIERTNHEDSD-----KD-HSFLTND 2158  
QY 168 LTOAQRPLIFNSSASAMDCINTLO-----KKEELDIREFLEBOMTLPPDFNS 220  
DB 2159 LAVPVAVKLPESGKYTGANKSVIRVRLGDLGIPSKLEENQELKPLDQCL----- 2212  
QY 221 GNTLQNDKRRYRDLIPYDSTRVPLGKNDYINASYIRIYNHEEYFIATQCPLETTIE 280  
DB 2213 GQTEENRRKRRYRDLIPYDSTRVPLGEGYINASFYIKIPVGEHEVYIATQCPLETTVG 2272  
QY 281 DEMQVLENNQNVAMITREIEGCVIKCYSTYPISTL-KEPLERHSPVLETFHVTQYFT 339  
DB 2273 DEMQVLENNQNVAMITREIEGCVIKCYSTYPISTL-KEPLERHSPVLETFHVTQYFT 2332

QY 340 VRVFOIVKSGTGKSCCVHLOFTKMPDHGTASADPFIKYRVYRKSHITGPLLHCSAG 399  
DB 2333 VRAMTLEDIQTRVNHISHLNFMTAPDHDTSPDPDLTFLISYRHHRSQPIITHCSAG 2392  
QY 400 VGRGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCMIQTEQOYOCYEIVLEVONL 459  
DB 2393 IGRSGTLICIDVVLGLISQDLFDISDLVRCMRQHRGMQTEBOYIFCYVILVYLTRL 2452  
QY 460 LA 461  
DB 2453 QA 2454

RESULT 5  
PCT-US94-09943-2  
Sequence 2, Application PC/TUS9409943  
GENERAL INFORMATION:

APPLICANT:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
TITLES OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL  
TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
STREET: 600 ATLANTIC AVENUE  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/09943  
FILING DATE: 01-SEP-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/115,573  
FILING DATE: 01-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: TWOMEY, MICHAEL J.  
REGISTRATION NUMBER: P-38,349  
REFERENCE/DOCKET NUMBER: L0461/7000MO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/720-3500  
TELEFAX: 617/720-2441  
TELEX: 92-1742 BZEKIEL  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2466 amino acids  
TYPES: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US94-09943-2

Query Match 26.2%; Score 639.5; DB 5; Length 2466;  
Best Local Similarity 37.8%; Pred. No. 1.6e-53;  
Matches 137; Conservative 62; Mismatches 128; Indels 35; Gaps 6;

QY 108 PEPLESDTDETVWVDSRLRNKNSMDETAAPSKTVSPVLSGSSRLSDTETSSEKE 167  
DB 2120 POKKTDDEITWG-NDELPIERTNHEDSD-----KD-HSFLTND 2158  
QY 168 LTOAQRPLIFNSSASAMDCINTLO-----KKEELDIREFLEBOMTLPPDFNS 220  
DB 2159 LAVPVAVKLPESGKYTGANKSVIRVRLGDLGIPSKLEENQELKPLDQCL----- 2212  
QY 221 GNTLQNDKRRYRDLIPYDSTRVPLGKNDYINASYIRIYNHEEYFIATQCPLETTIE 280  
DB 2213 GQTEENRRKRRYRDLIPYDSTRVPLGEGYINASFYIKIPVGEHEVYIATQCPLETTVG 2272  
QY 281 DEMQVLENNQNVAMITREIEGCVIKCYSTYPISTL-KEPLERHSPVLETFHVTQYFT 339  
DB 2273 DEMQVLENNQNVAMITREIEGCVIKCYSTYPISTL-KEPLERHSPVLETFHVTQYFT 2332

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Db 2213 GGTENRRKXKRYKILPYDARVPLGEGGYINASFIRKPGKEFYIAACQSPLETTVG 2272
Qy 281 DFMQVLENNCNVAMITREIECGVTKCYSWPISL-KEPLEFHHFVPLETHVTOYFT 339
Db 2273 DFMQVLENNCNVAMITREIECGVTKCYSWPISL-KEPLEFHHFVPLETHVTOYFT 2332
Qy 340 VRFVQIVKSTGSCQVCHLOFTKMPDHPGTPASADPFKIVRYVRSKSHITGPILVHCSAG 359
Db 2333 VRAMTLEDICTREVRHSHLFTAMPDHPDPSQPDLLFTISVHSHIRSGPIITHCSAG 2392
Qy 400 VGRGVFICVDVYFAIEKRYSPDINIVTQMKORCGMOTQEOYQCYEIVLEVLONT 459
Db 2393 IGRSGTLCIDVYGLISQDLDPDISLVRCRLQRHGMVQTEBDQYIFCYQVILVYLTRL 2452
Qy 460 LA 461
Db 2453 QA 2454
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RESULT 6
US-09-290-640-46
; Sequence 46, Application US/09290640
; Patent No. 6204055
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISFH-0351
; CURRENT APPLICATION NUMBER: US/09/290,640
; CURRENT FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 46
; LENGTH: 2485
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-290-640-46
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Query Match 26.2%; Score 639.5; DB 3; Length 2485;
Best Local Similarity 37.8%; Pred. No. 1.6e-53;
Matches 137; Conservative 62; Mismatches 128; Indels 35; Gaps 6;

Qy 108 PEPLSDTETVWDVDSLRNRKNSMDETAGPSKTVSPVLSGSSRLSKDTETSVSEKE 167
Db 2139 PQEKTDDEITWG-NDELPIERTNEDSD-----KD-HSFLINDE 2177
Qy 168 LITQAIQIRPLIFNSSARSAMDCLNTLQ-----KKEELDIIRFLELEQMTLPDDFNS 220
Db 2178 LAVLPVYKVLPSGKYTGANKSVIRVRLGLDQGISKELENLOELKELDQCLT----- 2231
Qy 221 GNTLQNRKRRYDILPYDSTRVPLGKNDYINASTIRVNHHEEFYIATQGPLPETIE 280
Db 2232 GQTKENRRKRYKILPYDARVPLGEGGYINASFIRKPGKEFYIAACQSPLETTVG 2291
Qy 281 DFMQVLENNCNVAMITREIECGVTKCYSWPISL-KEPLEFHHFVPLETHVTOYFT 339
Db 2232 DFMQVLENNCNVAMITREIECGVTKCYSWPISL-KEPLEFHHFVPLETHVTOYFT 2351
Qy 340 VRFVQIVKSTGSCQVCHLOFTKMPDHPGTPASADPFKIVRYVRSKSHITGPILVHCSAG 399
Db 2332 VRAMTLEDICTREVRHSHLFTAMPDHPDPSQPDLLFTISVHSHIRSGPIITHCSAG 2411
Qy 400 VGRGVFICVDVYFAIEKRYSPDINIVTQMKORCGMOTQEOYQCYEIVLEVLONT 459
Db 2412 IGRSGTLCIDVYGLISQDLDPDISLVRCRLQRHGMVQTEBDQYIFCYQVILVYLTRL 2471
Qy 460 LA 461
Db 2472 QA 2473
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```
US-09-665-615B-46
; Sequence 46, Application US/09665615B
; Patent No. 6653133
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; APPLICANT: Wyatt, Jacqueline
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISFH-0502
; CURRENT APPLICATION NUMBER: US/09/665,615B
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 46
; LENGTH: 2485
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-665-615B-46
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Query Match 26.2%; Score 639.5; DB 4; Length 2485;
Best Local Similarity 37.8%; Pred. No. 1.6e-53;
Matches 137; Conservative 62; Mismatches 128; Indels 35; Gaps 6;
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Qy 108 PEPLSDTETVWDVDSLRNRKNSMDETAGPSKTVSPVLSGSSRLSKDTETSVSEKE 167
Db 2139 PQEKTDDEITWG-NDELPIERTNEDSD-----KD-HSFLINDE 2177
Qy 168 LITQAIQIRPLIFNSSARSAMDCLNTLQ-----KKEELDIIRFLELEQMTLPDDFNS 220
Db 2178 LAVLPVYKVLPSGKYTGANKSVIRVRLGLDQGISKELENLOELKELDQCLT----- 2231
Qy 221 GNTLQNRKRRYDILPYDSTRVPLGKNDYINASTIRVNHHEEFYIATQGPLPETIE 280
Db 2232 GQTKENRRKRYKILPYDARVPLGEGGYINASFIRKPGKEFYIAACQSPLETTVG 2291
Qy 281 DFMQVLENNCNVAMITREIECGVTKCYSWPISL-KEPLEFHHFVPLETHVTOYFT 339
Db 2232 DFMQVLENNCNVAMITREIECGVTKCYSWPISL-KEPLEFHHFVPLETHVTOYFT 2351
Qy 340 VRFVQIVKSTGSCQVCHLOFTKMPDHPGTPASADPFKIVRYVRSKSHITGPILVHCSAG 399
Db 2332 VRAMTLEDICTREVRHSHLFTAMPDHPDPSQPDLLFTISVHSHIRSGPIITHCSAG 2411
Qy 400 VGRGVFICVDVYFAIEKRYSPDINIVTQMKORCGMOTQEOYQCYEIVLEVLONT 459
Db 2412 IGRSGTLCIDVYGLISQDLDPDISLVRCRLQRHGMVQTEBDQYIFCYQVILVYLTRL 2471
Qy 460 LA 461
Db 2472 QA 2473

RESULT 8
US-09-848-294-2
; Sequence 2, Application US/09848294
; Patent No. 6479640
; GENERAL INFORMATION:
; APPLICANT: Toms, Nicholas K.
; TITLE OF INVENTION: Isolation of A cDNA Encoding A No. 6479640el
; TITLE OF INVENTION: Protein Tyrosine Phosphatase Which Localizes to Focal
; FILE REFERENCE: CSHL90-04FZA
; CURRENT APPLICATION NUMBER: US/09/848,294
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 09/235,251
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 08/759,536
; PRIOR FILING DATE: 1996-12-04
; PRIOR APPLICATION NUMBER: 08/107,420
; PRIOR FILING DATE: 1993-08-16
; PRIOR APPLICATION NUMBER: 07/663,579
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PRIOR FILING DATE: 1991-03-01  
PRIOR APPLICATION NUMBER: 07/494,036  
PRIOR FILING DATE: 1990-03-14  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 913  
TYPE: PRT  
ORGANISM: Homosapiens  
US-09-848-294-2

Query Match 20.5%; Score 501; DB 4; Length 913;  
Best Local Similarity 37.4%; Pred. No. 1,8e-40;  
Matches 119; Conservative 44; Mismatches 110; Indels 45; Gaps 10;

QY 164 SEKITQIAQIRPIIFNSASASARDCL--NTLOKKEELDIRPLELEON-----212  
DB 607 SEDBINOL--FPEALFPMCPGCG--DTLEGMAOLKKLESGTVLIQFELYRKKGLAI 662  
QY 213 ---TLPDGNSGNTLQNRDKRYRDLIPDSTRVPIGKNKYINASYI-----RIYNH 262  
DB 663 TFAKLP-----QNDKRYKDVLPYDTRVLLQGNEDYINASYMEIPANLVNK 713  
QY 263 EEEVFIATQGPDETTEDFWQVLENNCNVIAITREIEGVAKCYSPISKEPLER 322  
DB 714 ----YIATQGPLPHTCAQFWVWDQKLSLIVMLTTLTERGRTKHQYWP---DPPDVW 765  
QY 323 EH--FSVLETFPHVQVTVAVFQIVKSTGKSCVCHLOFTKRPDHTPSADPFIKYV 380  
DB 766 NAGGFIHQCSDECIIVASKEMLVTNTQGEHVTTHLYVAMPDHGIPDSSDFLEPV 825  
QY 381 RYVERKSHI--TGPIIVHSGAGVGTGVCVDFVFSALIEKNTSPDINIVITQMRQRCMI 439  
DB 826 NYVASLAVDSBPVAVHGSAGIGRTGVAVTMTAMCLTERNLPIPLDIVRMQRQRAVY 885  
QY 440 QTKQYQPCYEVLEVYQ 457  
DB 886 QTSQYKFCVCAILRYVE 903

RESULT 9  
US-09-848-294-7  
Sequence 7, Application US/09848294  
Patent No. 6479640  
GENERAL INFORMATION:  
APPLICANT: Tunks, Nicholas K.  
TITLE OF INVENTION: Isolation of A CDNA Encoding A No. 6479640el  
TITLE OF INVENTION: Protein Tyrosine Phosphatase Which Localizes to Focal  
TITLE OF INVENTION: Adhesions and Uses Therefor  
FILE REFERENCE: CSHL90-04FZA  
CURRENT APPLICATION NUMBER: US/09/848,294  
PRIOR FILING DATE: 2001-05-03  
PRIOR APPLICATION NUMBER: 09/235,251  
PRIOR FILING DATE: 1999-01-22  
PRIOR APPLICATION NUMBER: 08/759,536  
PRIOR FILING DATE: 1996-12-04  
PRIOR APPLICATION NUMBER: 08/107,420  
PRIOR FILING DATE: 1993-08-16  
PRIOR APPLICATION NUMBER: 07/663,579  
PRIOR FILING DATE: 1991-03-01  
PRIOR APPLICATION NUMBER: 07/494,036  
PRIOR FILING DATE: 1990-03-14  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 7  
LENGTH: 244  
TYPE: PRT  
ORGANISM: Homosapiens  
US-09-848-294-7

Query Match 20.3%; Score 494; DB 4; Length 244;  
Best Local Similarity 41.7%; Pred. No. 1e-40;  
Matches 101; Conservative 38; Mismatches 85; Indels 18; Gaps 5;

QY 226 NPKNRRTDILPYDSTRVPIGKNKYINASYI-----RIYHBEFYIATQGPLERT 278  
DB 1 NLDKRRYKDVLPYDTRVLLQGNEDYINASYMEIPANLVNK-----YIATQGPLPHT 55  
QY 279 IEDFWQVLENNCNVIAITREIEGVAKCYSPISKEPLERH--FSVPLETFPHVQ 336  
DB 56 CAQFWQVWDQKLSLIVMLTTLTERGRTKHQYWP---DPPDVWNGGFFHQCSDECTI 112  
QY 337 YFTVRVPIVKSNGKSCVCHLOFTKMPDHTPSADPFIKYRYVERKSHI--TGPIIVH 395  
DB 113 AVYSREMLVTNTQGEHVTTHLYVAMPDHGIPDSSDFLEPVYVRSRVDSPEVLYVH 172  
QY 396 CSAGVGTGVCVDFVFSALIEKNTSPDINIVITQMRQRCMIQTKQYQPCYEVLEV 455  
DB 173 CSAGIGRTGVAVTMTAMCLTERNLPIPLDIVRMQRQRAVYQTSQYKFCVCAILRV 232  
QY 456 IQ 457  
DB 233 YE 234

RESULT 10  
US-08-348-006B-5  
Sequence 5, Application US/08348006B  
Patent No. 5658756  
GENERAL INFORMATION:  
APPLICANT: RODAN, GIDEON A.  
APPLICANT: SCHWIDT, AZRIEL  
APPLICANT: RUTLEDGE, SU JANE  
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASE  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSER: J. MARK HAND  
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000  
CITY: RAHWAY  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/348,006B  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/122,032  
FILING DATE: 14-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: HAND, J., MARK  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 189921A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-594-4720  
TELEFAX: 908-594-3905  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1911 amino acids  
TYPE: amino acid  
STRANDBESS: single  
TOPOLOGY: linear  
MOLECULAR TYPE: protein  
US-08-348-006B-5

Query Match 20.1%; Score 490.5; DB 1; Length 1911;  
Best Local Similarity 40.2%; Pred. No. 6.4e-39;  
Matches 107; Conservative 47; Mismatches 91; Indels 21; Gaps 7;  
QY 207 LELIQGTLFDD-----FNSGNTLQNRDKRYRDLIPYDSTRVPIG-----KXKDYINAS 255

Db 1643 MELEFKRLANSKXHTSRFISANLPCKKFNRLNIMPYESTWCLQPIRGVSGSDYINAS 1702  
Qy 256 YRIIVNHEEYFYIATOGPLPETIEDFMQWLENNCNIAMITREIEGVIKCYSPIS 315  
Db 1703 FID--GYROOKAVIATOGPLAETTEDFMRLMENNSTIVMLTKLREMGREKCHQYWP-- 1758  
Qy 316 LKEPLEFEHVSF--LTFHTVQYFVAVFOIVKSSQCYKHLQFTKMPDGTSPASAD 374  
Db 1759 AERSARQYFVVDPMABYNNPQYI-LREFKVTADAGQSRVTFQFOTDMEQGVPSGE 1817  
Qy 375 FFIKYRVYKSH---ITGPLLHCSAGVGRGVPICVAVFSALEKNTSPDINMIVTQ 430  
Db 1818 GFIDPIQVHTKEQFGQDGPISVHCSAGVGRGVFTLISVLERMYEGVVDIFQTVKM 1877  
Qy 431 MKKORCGMIQTKEQYQCYEIVLEVL 456  
Db 1878 LRTQRPAMVQTEDEYQFCYQALLEYL 1903

## RESULT 11

US-08-800-825A-5

Sequence 5, Application US/08800825A

Patent No. 5866397

GENERAL INFORMATION:

APPLICANT: RODAN, GIDEON A.

APPLICANT: SCHMIDT, AZRIEL

APPLICANT: RUTLEDGE, SU JANE

TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN

TITLE OF INVENTION: TYROSINE PHOSPHATASE

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: J. MARK HAND - MERCK &amp; CO., INC.

STREET: 126 E. LINCOLN AVE., P.O. BOX 2000

CITY: RAHWAY

STATE: NEW JERSEY

COUNTRY: USA

ZIP: 07065-0900

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/800,825A

FILING DATE: 14-FEB-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: HAND, J. MARK

REGISTRATION NUMBER: 36,545

REFERENCE/DOCKET NUMBER: 18992DA

TELECOMMUNICATION INFORMATION:

TELEPHONE: 732-594-3905

TELEFAX: 732-594-4720

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1911 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-800-825A-5

Query Match 20.1%; Score 490.5; DB 2; Length 1911;  
Best Local Similarity 40.2%; Pred. No. 6.4e-39;  
Matches 107; Conservative 47; Mismatches 91; Indels 21; Gaps 7;

Qy 207 LELEQWTLPPD-----FNSGNTLQNRDNRKYRDLIPYDSTRVPLG-----KXNDYINAS 255  
Db 1643 MELEFKRLANSKXHTSRFISANLPCKKFNRLNIMPYESTWCLQPIRGVSGSDYINAS 1702  
Qy 256 YRIIVNHEEYFYIATOGPLPETIEDFMQWLENNCNIAMITREIEGVIKCYSPIS 315

Db 1703 FID--GYROOKAVIATOGPLAETTEDFMRLMENNSTIVMLTKLREMGREKCHQYWP-- 1758  
Qy 316 LKEPLEFEHVSF--LTFHTVQYFVAVFOIVKSSQCYKHLQFTKMPDGTSPASAD 374  
Db 1759 AERSARQYFVVDPMABYNNPQYI-LREFKVTADAGQSRVTFQFOTDMEQGVPSGE 1817  
Qy 375 FFIKYRVYKSH---ITGPLLHCSAGVGRGVPICVAVFSALEKNTSPDINMIVTQ 430  
Db 1818 GFIDPIQVHTKEQFGQDGPISVHCSAGVGRGVFTLISVLERMYEGVVDIFQTVKM 1877  
Qy 431 MKKORCGMIQTKEQYQCYEIVLEVL 456  
Db 1878 LRTQRPAMVQTEDEYQFCYQALLEYL 1903

## RESULT 12

US-09-158-657-5

Sequence 5, Application US/09158657

Patent No. 6214564

GENERAL INFORMATION:

APPLICANT: RODAN, GIDEON A.

APPLICANT: SCHMIDT, AZRIEL

APPLICANT: RUTLEDGE, SU JANE

TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN

TITLE OF INVENTION: TYROSINE PHOSPHATASE

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: J. MARK HAND - MERCK &amp; CO., INC.

STREET: 126 E. LINCOLN AVE., P.O. BOX 2000

CITY: RAHWAY

STATE: NEW JERSEY

COUNTRY: USA

ZIP: 07065-0900

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/158,657

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/800,825

FILING DATE: 14-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: HAND, J. MARK

REGISTRATION NUMBER: 36,545

REFERENCE/DOCKET NUMBER: 18992DA

TELECOMMUNICATION INFORMATION:

TELEPHONE: 732-594-3905

TELEFAX: 732-594-4720

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1911 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-158-657-5

Query Match 20.1%; Score 490.5; DB 3; Length 1911;  
Best Local Similarity 40.2%; Pred. No. 6.4e-39;  
Matches 107; Conservative 47; Mismatches 91; Indels 21; Gaps 7;

Qy 207 LELEQWTLPPD-----FNSGNTLQNRDNRKYRDLIPYDSTRVPLG-----KXNDYINAS 255  
Db 1643 MELEFKRLANSKXHTSRFISANLPCKKFNRLNIMPYESTWCLQPIRGVSGSDYINAS 1702  
Qy 256 YRIIVNHEEYFYIATOGPLPETIEDFMQWLENNCNIAMITREIEGVIKCYSPIS 315  
Db 1703 FID--GYROOKAVIATOGPLAETTEDFMRLMENNSTIVMLTKLREMGREKCHQYWP-- 1758

QY 316 LKEPLERHSVF-LTEFVTVYVAVFQIVKSKTSQCVKHLQFTKPDHGT PASAD 374  
DB 1759 AERSARYQVYVVDPMAYNMPQYI-LREKVTADQDSRTTRQFOFTDMPGQVFKSGE 1817  
QY 375 FPIKYRYRYKSH-----ITGPLLVHCSAGVGRGVPCVDVVSALERNKSEPDIMNIYVQ 430  
DB 1818 GFIDFIGVHKTKEGFGQGPISVHCSAGVGRGVPTITLSIVLENNRYEGVVDIPQTVKM 1877  
QY 431 MKROCGMIGTQEQYQFCYEIVLEVL 456  
DB 1878 LRTQRPAMVQTEDEYQFCYQALLEYL 1903

## RESULT 13

PCT-US94-10166-5  
Sequence 5, Application PC/TUS9410166  
GENERAL INFORMATION:  
APPLICANT: RODAN, GIDEON A  
APPLICANT: SCHMIDT, AZRIEL  
APPLICANT: RUTLEDGE, SU JANE  
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASE  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JOHN W. WALLEN III  
STREET: P.O. BOX 2000, 126 E. LINCOLN AVE.  
CITY: RAHWAY  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065  
COMPUTER READABLE FORM:  
MEDIUM TYPE: IBM PC compatible  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/10166  
FILING DATE: 09-SEP-1994  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/122,032  
FILING DATE: 14-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WALLEN, JOHN W III  
REGISTRATION NUMBER: 35403  
REFERENCE/DOCKET NUMBER: 18992  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-594-3905  
TELEFAX: 908-594-4720  
TELEX: 138825  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1911 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US94-10166-5

Query Match 20.1%; Score 490.5; DB 5; Length 1911;  
Best Local Similarity 40.2%; Pred. No. 6,4e-39;  
Matches 107; Conservative 47; Mismatches 91; Indels 21; Gaps 7;

QY 207 LELQWTLPPD-----FNSGNTLQNRDKRRYRDLIPYDSTRVPLG-----KMKDYINAS 255  
DB 1643 MELERKLANSKAHNRSFISANLPCCKKFKRLVNIIMPVESTVVCQPIRGVSGSYINAS 1702  
QY 256 YIRIVNHEEYFIATQGPLPSTIEDFKQVLENNCNVIMATIRIEGVIKCYISYIPIS 315  
DB 1703 FID--GYROCKAYIATQGLAETEDPFMKMLWENNSTIVMLTKLRMGREKCHQYWP-- 1758  
QY 316 LKEPLERHSVF-LTEFVTVYVAVFQIVKSKTSQCVKHLQFTKPDHGT PASAD 374

DB 1759 AERSARYQVYVVDPMAYNMPQYI-LREKVTADQDSRTTRQFOFTDMPGQVFKSGE 1817  
QY 375 FPIKYRYRYKSH-----ITGPLLVHCSAGVGRGVPCVDVVSALERNKSEPDIMNIYVQ 430  
DB 1818 GFIDFIGVHKTKEGFGQGPISVHCSAGVGRGVPTITLSIVLENNRYEGVVDIPQTVKM 1877  
QY 431 MKROCGMIGTQEQYQFCYEIVLEVL 456  
DB 1878 LRTQRPAMVQTEDEYQFCYQALLEYL 1903

## RESULT 14

US-08-446-345-37  
Sequence 37, Application US/08446345  
Patent No. 5831009  
GENERAL INFORMATION:  
APPLICANT: Ullrich, Axel  
APPLICANT: Molier, Niels P.H.  
APPLICANT: Molier, Karin B.  
TITLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE  
TITLE OF INVENTION: PHOSPHATASES PTP-D1  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: N.Y.  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,345  
FILING DATE: 22-MAY-1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/234,440  
FILING DATE: 28-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30742  
REFERENCE/DOCKET NUMBER: 7683-054  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 231 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-446-345-37

Query Match 20.0%; Score 489; DB 2; Length 231;  
Best Local Similarity 42.0%; Pred. No. 2.9e-40;  
Matches 100; Conservative 37; Mismatches 83; Indels 18; Gaps 5;

QY 226 NRDKRYRVDIPYDSTRVPLGKNDYINASYI-----RIVNHEEYFIATQGPLPET 278  
DB 1 NLDKRRYKDVLPYDTTTLVLQGNEDYINASYNNHEIPANLVNK-----YIATQGPLPHT 55  
QY 279 IEDFWQVLENNCNVIMATIRIEGVIKCYISYIPISLKEPLERH--FSVLETFVTVQ 336  
DB 56 CAQFQVYVWQKSLIYMLTTLIFERGRKCHQYWP--DPPDVNHHGAFHQCSEDCIT 112  
QY 337 YFTVRVQIVKSKTSQCVKHLQFTKPDHGT PASADFPKYRYRYKSHI--IGPLLVH 395  
DB 113 AYVSRMLVNTVQTGEBHTVTLQYVAMPDHGLDDSDPLEFVNVYSLRVDSPLVH 172

QY 396 CSAGVGTGTCVFCVAVSAIEKNYSFDIANITVTGMRKQRCMTQTKQYQFCYEVIL 453  
DB 173 CSAGIGRTGVLTWMTAMCTERNLPYPLDIVRKRQDRAAMVQTSQYFVCEAL 230

## RESULT 15

US-08-685-992-21  
Sequence 21, Application US/08685992

Patent No. 5912138

GENERAL INFORMATION:

APPLICANT: Tonks, Nicholas

APPLICANT: Flint, Andrew J

TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN

TITLE OF INVENTION: TYROSINE PHOSPHATASES

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

STREET: Two Malitia Drive

CITY: Lexington

STATE: MA

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/685,992

FILING DATE: 25-JUL-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: CSHL96-03

TELECOMMUNICATION INFORMATION:

TELEPHONE: 781-861-6240

TELEFAX: 781-861-9540

TELEX:

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 242 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-685-992-21

Query Match

Best Local Similarity 41.8%; Score 487; DB 2; Length 242;

Matches 102; Conservative 37; Mismatches 79; Indels 26; Gaps 7;

QY 225 QNRKRNRYDILPYDSTRVPLGKKNKYINASYI-----RIVNHEEYFIATQGPLP 277

DB 11 QNLDKRNRYKQVLPYDSTRVPLGKKNKYINASYI-----RIVNHEEYFIATQGPLP 65

QY 278 TIEDFMQVLENNNCNVAMITREIECGVICKYSWPISTLKEPLEFEHPSVLETFHV--- 334

DB 66 TCAQFQVYVMDQKSLIVMLTTLTERGRTKQYWP---DEPDVANHGS-----PHIQOQ 117

QY 335 TQYFTVAVFQ--IVKSGTSGQCVKHLQFTKPDHGTASADFFIKYRYVRKSHI-TGP 391

DB 118 SEDCTIAYVSMVLTNTQTGESEHTVTHLQYVAMPDHGIPDSSDFLEFVNTYVRSIRVDS 177

QY 392 LLYVCSAGVARTGVFCVAVSAIEKNYSFDIANITVTQMRKQRCMTQTKQYQFCYEV 451

DB 178 VLVHCSAGIGRTGVLTWMTAMCTERNLPYPLDIVRKRQDRAAMVQTSQYFVCEA 237

QY 452 VLEV 455

DB 238 ILRV 241

Search completed: June 18, 2004, 19:41:11  
Job time : 25 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:40:09 ; Search time 49 seconds  
(without alignments)  
2667.576 Million cell updates/sec

Title: US-09-095-478a-6

Perfect score: 2439  
Sequence: 1 MSSSPKRVKRGKTRNDSEEG.....QYQCYEIVLEVIQNTIALY 463

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 28233646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2439	100.0	463	10	US-09-095-478-2
2	2212.5	90.7	426	10	US-09-095-478-1
3	2104.5	86.3	412	10	US-09-095-478-3
4	1997	81.9	379	10	US-09-095-478-8
5	1862	76.3	354	10	US-09-095-478-6
6	1378.5	56.5	420	16	US-10-311-764-4
7	668	27.4	122	10	US-09-095-478-4
8	644.5	26.4	381	10	US-09-095-478-7
9	640	26.2	1267	12	US-10-060-065-35
10	639.5	26.2	1267	14	US-10-059-585-56
11	639.5	26.2	358	10	US-09-095-478-9
12	639.5	26.2	2466	14	US-10-177-980-12
13	639.5	26.2	2485	9	US-09-802-669-46
14	639.5	26.2	2485	12	US-10-613-220-46
15	633.5	26.2	2485	16	US-10-408-765A-1349

16	581.5	23.8	263	12	US-10-087-684-93	Sequence 93, Appl
17	581.5	23.8	263	12	US-10-218-779-93	Sequence 93, Appl
18	566	23.2	132	10	US-09-095-478-5	Sequence 5, Appl
19	538	22.1	235	12	US-10-087-684-94	Sequence 94, Appl
20	538	22.1	235	12	US-10-218-779-94	Sequence 94, Appl
21	538	22.1	235	12	US-10-072-012-819	Sequence 819, App
22	501	20.5	913	9	US-09-848-294-2	Sequence 2, Appl
23	501	20.5	913	14	US-10-293-231-2	Sequence 36, Appl
24	501	20.5	913	15	US-10-366-547-38	Sequence 55, Appl
25	496.5	20.4	1948	9	US-09-808-602-55	Sequence 36, Appl
26	496.5	20.4	1948	10	US-09-800-198-45	Sequence 45, Appl
27	494	20.3	244	9	US-09-848-294-7	Sequence 7, Appl
28	494	20.3	244	14	US-10-293-231-7	Sequence 54, Appl
29	490.5	20.1	1502	9	US-09-808-602-54	Sequence 44, Appl
30	490.5	20.1	1502	10	US-10-366-547-40	Sequence 44, Appl
31	490	20.1	703	15	US-10-366-547-40	Sequence 44, Appl
32	487	20.0	281	9	US-09-788-626-22	Sequence 2, Appl
33	487	20.0	1337	14	US-10-390-501-2	Sequence 2, Appl
34	487	20.0	1337	15	US-10-366-547-42	Sequence 42, Appl
35	487	20.0	1337	15	US-10-366-547-44	Sequence 42, Appl
36	484	19.8	1156	15	US-10-369-493-6128	Sequence 6128, Ap
37	483.5	19.8	1439	12	US-09-887-669-2	Sequence 2, Appl
38	483.5	19.8	1439	16	US-10-408-765A-284	Sequence 284, App
39	482.5	19.8	264	14	US-10-245-539-6	Sequence 6, Appl
40	481.5	19.7	344	16	US-10-408-765A-1670	Sequence 1670, Ap
41	481.5	19.7	1463	14	US-10-176-847-22	Sequence 22, Appl
42	481.5	19.7	1463	14	US-10-205-823-343	Sequence 343, App
43	479.5	19.6	1495	15	US-10-258-666-12	Sequence 12, Appl
44	477.5	19.6	1457	12	US-09-887-669-1	Sequence 1, Appl
45	476	19.5	1216	15	US-10-366-547-49	Sequence 49, Appl

#### ALIGNMENTS

RESULT 1  
US-09-095-478-2  
Sequence 2, Application US/09095478  
Publication No. US20030095970A1  
GENERAL INFORMATION:  
APPLICANT: Plozman, Gregory  
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE SUPPOS AND  
TITLE OF INVENTION: RELATED PRODUCTS AND  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 613 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FASTSEQ for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/095,478  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 224/115  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440  
 TELE: 67-3510  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 463 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 US-09-095-478-2

Query Match 100.0%; Score 2439; DB 10; Length 463;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-215;  
 Matches 463; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSPKRYGKTGRDNDDEEGNSGNLNLNSLPSSSQKMTPTKPYQNKMLKYEHLIDLM 60  
 DB 1 MSSPKRYGKTGRDNDDEEGNSGNLNLNSLPSSSQKMTPTKPYQNKMLKYEHLIDLM 60  
 QY 61 VFLLIKTIWVVFPLMKKGLIFGNKNSENVKPSHHLSFSDKXELVYPPLESIDTETW 120  
 DB 61 VFLLIKTIWVVFPLMKKGLIFGNKNSENVKPSHHLSFSDKXELVYPPLESIDTETW 120  
 QY 121 DVSDRLNRKNSMDSETAGPSKTVPVLSGSSRLSKOTETSSEKELTOLAQIRPLIFN 180  
 DB 121 DVSDRLNRKNSMDSETAGPSKTVPVLSGSSRLSKOTETSSEKELTOLAQIRPLIFN 180  
 QY 181 SSARSAMDCLNTLQCKEELDIIRFPLEQMTLPDDFNSGNTLQNRDKRYDILPYDS 240  
 DB 181 SSARSAMDCLNTLQCKEELDIIRFPLEQMTLPDDFNSGNTLQNRDKRYDILPYDS 240  
 QY 241 TRVPLGNKNDYINASTIRIVNHEEYFYATQGLPETIEDFMQVLENNCNVIAITRE 300  
 DB 241 TRVPLGNKNDYINASTIRIVNHEEYFYATQGLPETIEDFMQVLENNCNVIAITRE 300  
 QY 301 IECGVIKCYSWPISLKEPLFEHFSVPLETFHTVQYFTVAVFOIVKSTGSKQCVHQLQ 360  
 DB 301 IECGVIKCYSWPISLKEPLFEHFSVPLETFHTVQYFTVAVFOIVKSTGSKQCVHQLQ 360  
 QY 361 FTWPDHGTSPASADPFIKYRYVRKSHITGPLLHSCSAGVGRGVFTICDVVPSAIEKNY 420  
 DB 361 FTWPDHGTSPASADPFIKYRYVRKSHITGPLLHSCSAGVGRGVFTICDVVPSAIEKNY 420  
 QY 421 SFDIMNIVTQMRKRCGMIOFKEQYOFCEIYVLEVLQNLITALLY 463  
 DB 421 SFDIMNIVTQMRKRCGMIOFKEQYOFCEIYVLEVLQNLITALLY 463

RESULT 2  
 US-09-095-478-1  
 ; Sequence 1, Application US/09095478  
 ; Publication No. US20030095970A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Plozman, Gregory  
 ; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
 ; TITLE OF INVENTION: PHOSPHATASE SUPPOS AND  
 ; TITLE OF INVENTION: RELATED PRODUCTS AND  
 ; TITLE OF INVENTION: METHODS  
 ; NUMBER OF SEQUENCES: 25  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; STREET: Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071-2066  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: FastSeq for Windows 2.0

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/095,478  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard J.  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 224/115  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELE: 67-3510  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 426 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 US-09-095-478-1

Query Match 90.7%; Score 2212.5; DB 10; Length 426;  
 Best Local Similarity 92.0%; Pred. No. 1.2e-194;  
 Matches 426; Conservative 0; Mismatches 0; Indels 37; Gaps 1;

QY 1 MSSPKRYGKTGRDNDDEEGNSGNLNLNSLPSSSQKMTPTKPYQNKMLKYEHLIDLM 60  
 DB 1 MSSPKRYGKTGRDNDDEEGNSGNLNLNSLPSSSQKMTPTKPYQNKMLKYEHLIDLM 60  
 QY 61 VFLLIKTIWVVFPLMKKGLIFGNKNSENVKPSHHLSFSDKXELVYPPLESIDTETW 120  
 DB 61 VFLLIKTIWVVFPLMKKGLIFGNKNSENVKPSHHLSFSDKXELVYPPLESIDTETW 120  
 QY 44 -----IFGNKNSENVKPSHHLSFSDKXELVYPPLESIDTETW 83  
 DB 44 -----IFGNKNSENVKPSHHLSFSDKXELVYPPLESIDTETW 83  
 QY 121 DVSDRLNRKNSMDSETAGPSKTVPVLSGSSRLSKOTETSSEKELTOLAQIRPLIFN 180  
 DB 121 DVSDRLNRKNSMDSETAGPSKTVPVLSGSSRLSKOTETSSEKELTOLAQIRPLIFN 180  
 QY 84 DVSDRLNRKNSMDSETAGPSKTVPVLSGSSRLSKOTETSSEKELTOLAQIRPLIFN 143  
 DB 84 DVSDRLNRKNSMDSETAGPSKTVPVLSGSSRLSKOTETSSEKELTOLAQIRPLIFN 143  
 QY 181 SSARSAMDCLNTLQCKEELDIIRFPLEQMTLPDDFNSGNTLQNRDKRYDILPYDS 240  
 DB 181 SSARSAMDCLNTLQCKEELDIIRFPLEQMTLPDDFNSGNTLQNRDKRYDILPYDS 240  
 QY 144 SSARSAMDCLNTLQCKEELDIIRFPLEQMTLPDDFNSGNTLQNRDKRYDILPYDS 203  
 DB 144 SSARSAMDCLNTLQCKEELDIIRFPLEQMTLPDDFNSGNTLQNRDKRYDILPYDS 203  
 QY 241 TRVPLGNKNDYINASTIRIVNHEEYFYATQGLPETIEDFMQVLENNCNVIAITRE 300  
 DB 241 TRVPLGNKNDYINASTIRIVNHEEYFYATQGLPETIEDFMQVLENNCNVIAITRE 300  
 QY 204 TRVPLGNKNDYINASTIRIVNHEEYFYATQGLPETIEDFMQVLENNCNVIAITRE 263  
 DB 204 TRVPLGNKNDYINASTIRIVNHEEYFYATQGLPETIEDFMQVLENNCNVIAITRE 263  
 QY 301 IECGVIKCYSWPISLKEPLFEHFSVPLETFHTVQYFTVAVFOIVKSTGSKQCVHQLQ 360  
 DB 301 IECGVIKCYSWPISLKEPLFEHFSVPLETFHTVQYFTVAVFOIVKSTGSKQCVHQLQ 360  
 QY 264 IECGVIKCYSWPISLKEPLFEHFSVPLETFHTVQYFTVAVFOIVKSTGSKQCVHQLQ 323  
 DB 264 IECGVIKCYSWPISLKEPLFEHFSVPLETFHTVQYFTVAVFOIVKSTGSKQCVHQLQ 323  
 QY 361 FTWPDHGTSPASADPFIKYRYVRKSHITGPLLHSCSAGVGRGVFTICDVVPSAIEKNY 420  
 DB 361 FTWPDHGTSPASADPFIKYRYVRKSHITGPLLHSCSAGVGRGVFTICDVVPSAIEKNY 420  
 QY 324 FTWPDHGTSPASADPFIKYRYVRKSHITGPLLHSCSAGVGRGVFTICDVVPSAIEKNY 383  
 DB 324 FTWPDHGTSPASADPFIKYRYVRKSHITGPLLHSCSAGVGRGVFTICDVVPSAIEKNY 383  
 QY 421 SFDIMNIVTQMRKRCGMIOFKEQYOFCEIYVLEVLQNLITALLY 463  
 DB 421 SFDIMNIVTQMRKRCGMIOFKEQYOFCEIYVLEVLQNLITALLY 463  
 QY 384 SFDIMNIVTQMRKRCGMIOFKEQYOFCEIYVLEVLQNLITALLY 426  
 DB 384 SFDIMNIVTQMRKRCGMIOFKEQYOFCEIYVLEVLQNLITALLY 426

RESULT 3  
 US-09-095-478-3  
 ; Sequence 3, Application US/09095478  
 ; Publication No. US20030095970A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Plozman, Gregory  
 ; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
 ; TITLE OF INVENTION: PHOSPHATASE SUPPOS AND  
 ; TITLE OF INVENTION: RELATED PRODUCTS AND  
 ; TITLE OF INVENTION: METHODS  
 ; NUMBER OF SEQUENCES: 25  
 ; CORRESPONDENCE ADDRESS:

```

ADDRESS: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
US-09-095-478-3

Query Match      86.3%; Score 2104.5; DB 10; length 412;
Best Local Similarity 91.6%; Pred. No. 9,66-185;
Matches 405; Conservative 0; Mismatches 0; Indels 37; Gaps 1;

QY 1 MSSPRKYGKGTGRNDEEGNSGNTLRNLSLPSSSQKMTPTKPYQNNLMKVEEHLILM 60
DB 1 MSSPRKYGKGTGRNDEEGNSGNTLRNLSLPSSSQKMTPTKPYQNNLMKVEEHLILM 60
QY 61 VFLLIKTIWTVFPLMGKLIFGKNSKSNKPSHHLSFSDKTELVYPEPLESDPTETW 120
DB 44 -----IFGNHNSKSNKPSHHLSFSDKTELVYPEPLESDPTETW 83
QY 121 DVSDRSIRNRNNSMDSETAPGSKTVSPVLSGSSSLSKDTETVSSEKELTOLAQIRPLIFN 180
DB 84 DVSDRSIRNRNNSMDSETAPGSKTVSPVLSGSSSLSKDTETVSSEKELTOLAQIRPLIFN 143
QY 181 SSARSARNDCLNTLOKKEELDIIRPLELBQMTLPDDFNSGNTLQNRDKRYDILPYDS 240
DB 144 SSARSARNDCLNTLOKKEELDIIRPLELBQMTLPDDFNSGNTLQNRDKRYDILPYDS 203
QY 241 TRVPLGKNDKYINASYRIYNHSEEVYIATQGPLPETIIDFQMTLNNCNVIAITTE 300
DB 204 TRVPLGKNDKYINASYRIYNHSEEVYIATQGPLPETIIDFQMTLNNCNVIAITTE 263
QY 301 IEGGVKCYSYNPISLKEPLEFSEFVLETFHVTQYFTVRVQIYKKSQCVKHLQ 360
DB 264 IEGGVKCYSYNPISLKEPLEFSEFVLETFHVTQYFTVRVQIYKKSQCVKHLQ 323
QY 361 FTGPHGTPASADFTIKYRYRKSHITQPLLVHGSAGRGVTCVDVYPSAIEKNY 420
DB 324 FTGPHGTPASADFTIKYRYRKSHITQPLLVHGSAGRGVTCVDVYPSAIEKNY 383
QY 421 SFDINNIIVTQMRKQRCGMQTK 442
DB 384 SFDINNIIVTQMRKQRCGMQTK 405

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RESULT 4
US-09-095-478-8
; Sequence 8, Application US/09095478
; Publication No. US20030095970A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE SUBTYPES AND
; TITLE OF INVENTION: RELATED PRODUCTS AND
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 379 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-09-095-478-8

Query Match      81.9%; Score 1997; DB 10; length 379;
Best Local Similarity 100.0%; Pred. No. 6,66-175;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 GKNKSNKPSHHLSFSDKTELVYPEPLESDPTETWVSDRSIRNRNNSMDSETAPGS 142
DB 1 GKNKSNKPSHHLSFSDKTELVYPEPLESDPTETWVSDRSIRNRNNSMDSETAPGS 60
QY 143 KTVSPVLSGSSSLSKDTETVSSEKELTOLAQIRPLIFNSARSARNDCLNTLOKKEELDI 202
DB 61 KTVSPVLSGSSSLSKDTETVSSEKELTOLAQIRPLIFNSARSARNDCLNTLOKKEELDI 120
QY 203 IREPLELBQMTLPDDFNSGNTLQNRDKRYDILPYDSRVPLGKNDKYINASYRIYNH 262
DB 121 IREPLELBQMTLPDDFNSGNTLQNRDKRYDILPYDSRVPLGKNDKYINASYRIYNH 180
QY 263 EEEFYIATQGPLPETIIDFQMTLNNCNVIAITTEIEGVKCYSYNPISLKEPLEF 322
DB 181 EEEFYIATQGPLPETIIDFQMTLNNCNVIAITTEIEGVKCYSYNPISLKEPLEF 240
QY 323 EHFVLETFHVTQYFTVRVQIYKKSQCVKHLQFTKMPDHGTBASADFTIKYRY 382
DB 241 EHFVLETFHVTQYFTVRVQIYKKSQCVKHLQFTKMPDHGTBASADFTIKYRY 300

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QY 383 VAKSHITGPELVHCSAGVGRVTFICVDVFSALIKRNSFDIMNIVTQMRKRCGMIQTK 442  
DB 301 VAKSHITGPELVHCSAGVGRVTFICVDVFSALIKRNSFDIMNIVTQMRKRCGMIQTK 360  
QY 443 BOYOCYBETVLEVLQNL 461  
DB 361 BOYOCYBETVLEVLQNL 379

## RESULT 5

US-09-095-478-6  
; Sequence 6, Application US/09095478  
; Publication No. US20030095970A1  
; GENERAL INFORMATION:  
; APPLICANT: PLOWMAN, Gregory  
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
; TITLE OF INVENTION: PHOSPHATASE SUPPOS AND  
; TITLE OF INVENTION: RELATED PRODUCTS AND  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FASTSEQ for windows 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/095,478  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 224/115  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 354 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Peptide  
US-09-095-478-6

Query Match 76.3%; Score 1862; DB 10; Length 354;

Best Local Similarity 100.0%; Pred. No. 1,6e-162; Indels 0; Gaps 0;

Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 PEPLESDTDETVWDVSDRLRNKNSMDSETAGPSKTVSPVLSGSSRLSKDTETSVSEKE 167  
DB 1 PEPLESDTDETVWDVSDRLRNKNSMDSETAGPSKTVSPVLSGSSRLSKDTETSVSEKE 60  
QY 168 LTGLAQIPELIFNSARSGAMDCLNTLQKEELDIIRFLEEQMTLPDDPNSGTLQNR 227  
DB 61 LTGLAQIPELIFNSARSGAMDCLNTLQKEELDIIRFLEEQMTLPDDPNSGTLQNR 120  
QY 228 DKNRYDILPYDSTVPLGKNQDYINASYIRIVNHEEYFIATQGPLPFIETEDFWQVVL 287

DB 121 DKNRYDILPYDSTVPLGKNQDYINASYIRIVNHEEYFIATQGPLPFIETEDFWQVVL 180  
QY 288 ENNCNVAMITREBQGVICYSYMPISLKEPFEHESVLEFPHTQVFTVRVPIYK 347  
DB 181 ENNCNVAMITREBQGVICYSYMPISLKEPFEHESVLEFPHTQVFTVRVPIYK 240  
QY 348 KSTGKSQCVKHLQFTKMPDGHGTPASADFFIKYRYVAKSHITGPELVHCSAGVGRVTFI 407  
DB 241 KSTGKSQCVKHLQFTKMPDGHGTPASADFFIKYRYVAKSHITGPELVHCSAGVGRVTFI 300  
QY 408 CVDVFSALIKRNSFDIMNIVTQMRKRCGMIQTKBOYOCYBETVLEVLQNL 461  
DB 301 CVDVFSALIKRNSFDIMNIVTQMRKRCGMIQTKBOYOCYBETVLEVLQNL 354

## RESULT 6

US-10-311-764-4  
; Sequence 4, Application US/10311764  
; Publication No. US20040023245A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.; AU-YOUNG, Janice K.  
; APPLICANT: BAUGHN, Mariah R.; DING, Li  
; APPLICANT: ELIOTT, Vicki S.; GANDHI, Ameena R.  
; APPLICANT: GRIFFIN, Jennifer A.; HAPALIA, April J.A.  
; APPLICANT: KARNNEY, Liam, LEE, Ernestine A.  
; APPLICANT: LU, Yan, NGUYEN, Daniel B.  
; APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi  
; APPLICANT: REDDY, Roopa M.; SANJANMALA, Madhusudan M.  
; APPLICANT: STEWART, Elizabeth A.; TANG, Y. Tom  
; APPLICANT: THEORNTON, Michael B.; TRIBOULEY, Catherine M.  
; APPLICANT: CHAMLA, Narinder K.; YANG, Junming  
; APPLICANT: YAO, Monique G.; YUE, Henry  
; TITLE OF INVENTION: PROTEIN PHOSPHATASES  
; FILE REFERENCE: PI-0126 USN  
; CURRENT APPLICATION NUMBER: US/10/311,764  
; CURRENT FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: PCT/US01/19442  
; PRIOR FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: US 60/212,447  
; PRIOR FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: US 60/213,746  
; PRIOR FILING DATE: 2000-06-22  
; PRIOR APPLICATION NUMBER: US 60/215,210  
; PRIOR FILING DATE: 2000-06-29  
; PRIOR APPLICATION NUMBER: US 60/216,529  
; PRIOR FILING DATE: 2000-07-06  
; PRIOR APPLICATION NUMBER: US 60/218,080  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/220,117  
; PRIOR FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PERL Program  
; SEQ ID NO 4  
; LENGTH: 420  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20040023245A1 7476861CD1  
US-10-311-764-4

Query Match 56.5%; Score 1378.5; DB 16; Length 420;

Best Local Similarity 59.2%; Pred. No. 6.1e-118; Indels 45; Gaps 3;

Matches 274; Conservative 52; Mismatches 92; Indels 45; Gaps 3;

QY 1 MSSPRKRGKGTGDNDEBBSGNTLNRNLSGSSQOMPTKTVQKNTLKKYEHLILM 60  
DB 1 MSSPRDRAPAPVDYENDEADLAFRETLPSSQGNTRYKTV----- 44  
QY 61 VPLLKTIWYVFKLWKKGLIPGNKNSENVKSHLSFSDKYELVYPEPLESDTDETVW 120  
DB 45 -----FENKYNSEKVKLTFANFPHNDYEDVEFEPESGSDPSMW 83



Db 1 PDELATMEAPBEGDITD---YDGSPLPEVPEVSSEGGKVDLALSLTAASQREKPEIEDA 57  
 QY 153 SRLSKD--TETS-----VSEKELTOLAQRPLIFNSASAMRDLANTLQ----- 195  
 Db 58 TQESANSSTETITDGEDSSKDPPLTNBELALPVYRVPSSGKYTGTOUATRTIQGLD 117  
 QY 196 ---KXEBLDIREFLEBQMTLPDDFNSGNTLQNDKRRYRDLIPYDSTRVPLGKNKIY 252  
 Db 118 QGIPKXELMLOBLKPLDQCLT-----GQTKENRRKRYKXILIPYDTRVPLGDEGGYI 171  
 QY 253 NASYRIVNHEBEYFIATQGPLPEIIEFKQMWLENNQNVNMTREIEGCVKCYSYW 312  
 Db 172 NASFRIRIPGTQEPFYIACQPLPTTQDFFQMWQNSVTIAMTQVEGSKLKQRYW 231  
 QY 313 PLSL--KEPLFEHFSVLETFYVTOYFTYVPOIYKSKTSQCVKHLQFTKMPDHGTPA 371  
 Db 232 PSLIGTTTANERLRLALRMQGLKGFIVRVVALLDIOGVEYRHISHLNFTAMPDHDPS 291  
 QY 372 SAD---FPIKYRYRYRKSHITGPPLVHGSAGYRGVPCVDVVSALIKYSPIMNIY 428  
 Db 292 QPDDLITFISYMRHRRS---GPVITHCSAGIGRGTILCIDVVLGILSODLEFDISLV 348  
 QY 429 TQWRKQRCGMIOQTEKQYQFCYEVLEVLQNLTA 461  
 Db 349 RCMRLQRHGVQTEGQYVZCYGVILVLTQLA 361

RESULT 9  
 US-10-060-065-35  
 ; Sequence 35, Application US/10060065  
 ; Publication No. US20030017480A1  
 ; GENERAL INFORMATION:

APPLICANT: Toshio Ota  
 APPLICANT: Takao Isogai  
 APPLICANT: Tetsuo Nishikawa  
 APPLICANT: Koji Hayashi  
 APPLICANT: Kaoru Otsuka  
 APPLICANT: Jun-ichi Yamamoto  
 APPLICANT: Shizuko Ishii  
 APPLICANT: Tomoyasu Sugiyama  
 APPLICANT: Ai Wakamatsu  
 APPLICANT: Keiichi Nagai  
 APPLICANT: Tetsuji Otsuki  
 APPLICANT: Shin-ichi Funahashi  
 APPLICANT: Chiaki Senoo  
 APPLICANT: Jun-ichi Nezu  
 TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE  
 FILE REFERENCE: 06501-099002  
 CURRENT FILING DATE: US/10/060, 065  
 PRIOR APPLICATION NUMBER: PCT/JP00/05061  
 PRIOR FILING DATE: 2000-07-28  
 PRIOR APPLICATION NUMBER: US 60/159,590  
 PRIOR FILING DATE: 1999-10-18  
 PRIOR APPLICATION NUMBER: US 60/183,322  
 PRIOR FILING DATE: 2000-02-17  
 PRIOR APPLICATION NUMBER: JP 11-248036  
 PRIOR FILING DATE: 1999-07-29  
 PRIOR APPLICATION NUMBER: JP 2000-118776  
 PRIOR FILING DATE: 2000-01-11  
 PRIOR APPLICATION NUMBER: JP 2000-183767  
 PRIOR FILING DATE: 2000-05-02  
 PRIOR APPLICATION NUMBER: JP 2000-241899  
 PRIOR FILING DATE: 2000-06-09  
 NUMBER OF SEQ ID NOS: 43  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 35  
 LENGTH: 1267  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-060-065-35

Query Match 26.2%; Score 640; DB 12; Length 1267;

Best Local Similarity 38.0%; Pred. No. 2,7e-49;  
 Matches 137; Conservative 62; Mismatches 128; Indels 34; Gaps 6;  
 QY 108 PEPLESTDETVDVDSRLRNKNSDSETAGSKTVSVLSSSSLSLSDTETSVSEKE 167  
 Db 922 PQEKTDDELTWG--NELPELERTNHDSD-----KD-HSELTNDE 960  
 QY 168 LTYOLAQRPLIFNSASAMRDLANTLQ-----KKEBLDIREFLEBQMTLPDDFNSG 221  
 Db 961 LAIVLPVVKVLPSSGKYTANLKSIVRLVARSGIPSELNLOKLPDQCLT-----G 1014  
 QY 222 NTLQNRKRYRDLIPDSTRVPLGKNKYDINASYIIVNHEBEYFIATQGPLPEIIE 281  
 Db 1015 QTKENRRKRYKXILIPYDTRVPLGDEGGYINAFIKIPGKEFVYIACQGPLPTTQD 1074  
 QY 282 FQWVLENNQNVNMTREIEGCVKCYSYWPLSL--KEPLFEHFSVLETFYVTOYFTV 340  
 Db 1075 FQWVLENNQNVNMTREIEGCVKCYSYWPLSL--KEPLFEHFSVLETFYVTOYFTV 1134  
 QY 341 RVPOIYKSKTSQCVKHLQFTKMPDHGTPASADPFIKYRYRYRKSHITGPPLVHGSAGV 400  
 Db 1135 RAMTLEDIQTRFVYRHISHLNFTAMPDHDTPSPDDDLITFISYMRHRRSGEILTHCSAGI 1194  
 QY 401 GRTGVPCVDVVSALIKYSPIMNIYQKRQROSCMIOQTEKQYQFCYEVLEVLQNL 460  
 Db 1195 GRSSTLTCIDVVLGILSODLEFDISLVRCRLQRHGVQTEGQYVZCYGVILVLTQL 1254  
 QY 461 A 461  
 Db 1255 A 1255

RESULT 10  
 US-10-059-585-56  
 ; Sequence 56, Application US/10059585  
 ; Publication No. US20030082776A1  
 ; GENERAL INFORMATION:

APPLICANT: Ota, Toshio  
 APPLICANT: Isogai, Takao  
 APPLICANT: Nishikawa, Tetsuo  
 APPLICANT: Hayashi, Koji  
 APPLICANT: Otsuka, Kaoru  
 APPLICANT: Yamamoto, Jun-ichi  
 APPLICANT: Ishii, Shizuko  
 APPLICANT: Sugiyama, Tomoyasu  
 APPLICANT: Wakamatsu, Ai  
 APPLICANT: Nagai, Keiichi  
 APPLICANT: Otsuki, Tetsuji  
 APPLICANT: Funahashi, Shin-ichi  
 APPLICANT: Senoo, Chiaki  
 APPLICANT: Nezu, Jun-ichi  
 TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE  
 FILE REFERENCE: 06501-098001  
 CURRENT FILING DATE: US/10/059, 585  
 PRIOR APPLICATION NUMBER: 2002-01-29  
 PRIOR APPLICATION NUMBER: PCT/JP00/05060  
 PRIOR FILING DATE: 2000-07-28  
 PRIOR APPLICATION NUMBER: US 60/183,322  
 PRIOR FILING DATE: 2000-02-17  
 PRIOR APPLICATION NUMBER: US 60/159,590  
 PRIOR FILING DATE: 1999-10-18  
 PRIOR APPLICATION NUMBER: JP 2000-118776  
 PRIOR FILING DATE: 2000-01-11  
 PRIOR APPLICATION NUMBER: JP 2000-183767  
 PRIOR FILING DATE: 2000-05-02  
 PRIOR APPLICATION NUMBER: JP 11-248036  
 PRIOR FILING DATE: 1999-07-29  
 NUMBER OF SEQ ID NOS: 64  
 SOFTWARE: PatsSeq for Windows Version 4.0  
 SEQ ID NO 56  
 LENGTH: 1267  
 TYPE: PRT

ORGANISM: Homo sapiens  
US-10-059-585-56

Query Match 26.2%; Score 640; DB 14; Length 1267;  
Best Local Similarity 38.0%; Pred. No. 2.7e-49;  
Matches 137; Conservative 62; Mismatches 128; Indels 34; Gaps 6;

QY 108 PEPLESDTDEVTWVDSRSLRNKMSMDETAGPSKTVSPVLSGSSRLSKDTETVSKE 167  
DB 922 POKKTDDEITWG-NDELPIERTNHEDSD-----KD-HSFLTNDE 960  
QY 168 LITQAQIRPLIFNSSARSAMDCLNTLQ-----KKEHDIIREFLIEQMTLPDDFNSG 221  
DB 961 LAVLPVVKVLPSCGYTGANKSVIRLVARSIGPSKLEMLQELKPLDQCLT-----G 1014  
QY 222 NTLQNRDKRRYRDILPYDSTRVPLGKNQDYINASTIRIVNHEEYFYIAQGLPFTIED 281  
DB 1015 QTKERRRRKRYKNILPYDSTRVPLGDEGGYINASTIRIVNHEEYFYIAQGLPFTIYGD 1074  
QY 282 FWMQVLNNNCVIAITREIECGVTKCYSYWPIST-KEPLEPEHPSVLETFHTVQYFTV 340  
DB 1075 FWMQWEKSTYIAMTQVEBEKIKQRYWPNILGKTMTWSNRLALVPMQQLGKGV 1134  
QY 341 RVFOIVKSTGSKQCVKHLQFTKMPDHCPTASADFFIKYRVYKSHITGSLVHCSAGV 400  
DB 1135 RAMTLEDIOTREVRHSHLFTAMPDHDTPSQPDLLTFISYMRHIRSGPIITHCSAGI 1194  
QY 401 GRITGVICVDVYFSAIEKNYSFDIMNITQMKRCGMIOKEQYQCYEIVLEVLQNTL 460  
DB 1195 GRSGLTICIDVVLGISQDLDPDIDSLVRCMLQGRHGWQTDQYFCYQVILVLTRELQ 1254  
QY 461 A 461  
DB 1255 A 1255

RESULT 11  
US-09-095-478-9

Sequence 9, Application US/09095478  
Publication No. US20030095970A1

GENERAL INFORMATION:

APPLICANT: PLOWMAN, Gregory  
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND  
TITLE OF INVENTION: RELATED PRODUCTS AND  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Pith Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: Storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FASTSEQ for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/095.478  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 224/115  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440

INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 358 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide

US-09-095-478-9  
Query Match 26.2%; Score 639.5; DB 10; Length 358;  
Best Local Similarity 37.8%; Pred. No. 4.7e-50;  
Matches 137; Conservative 62; Mismatches 128; Indels 35; Gaps 6;

QY 108 PEPLESDTDEVTWVDSRSLRNKMSMDETAGPSKTVSPVLSGSSRLSKDTETVSKE 167  
DB 24 POKKTDDEITWG-NDELPIERTNHEDSD-----KD-HSFLTNDE 62  
QY 168 LITQAQIRPLIFNSSARSAMDCLNTLQ-----KKEHDIIREFLIEQMTLPDDFNS 220  
DB 63 LAVLPVVKVLPSCGYTGANKSVIRLVARSIGPSKLEMLQELKPLDQCLT----- 116  
QY 221 NTLQNRDKRRYRDILPYDSTRVPLGKNQDYINASTIRIVNHEEYFYIAQGLPFTIE 280  
DB 117 GQTKERRRRKRYKNILPYDSTRVPLGDEGGYINASTIRIVNHEEYFYIAQGLPFTIYGD 176  
QY 281 FWMQVLNNNCVIAITREIECGVTKCYSYWPIST-KEPLEPEHPSVLETFHTVQYFT 339  
DB 177 FWMQWEKSTYIAMTQVEBEKIKQRYWPNILGKTMTWSNRLALVPMQQLGKGV 236  
QY 340 RVFOIVKSTGSKQCVKHLQFTKMPDHCPTASADFFIKYRVYKSHITGSLVHCSAG 399  
DB 237 RAMTLEDIOTREVRHSHLFTAMPDHDTPSQPDLLTFISYMRHIRSGPIITHCSAG 296  
QY 400 VGRITGVICVDVYFSAIEKNYSFDIMNITQMKRCGMIOKEQYQCYEIVLEVLQNTL 459  
DB 297 IGRSGLTICIDVVLGISQDLDPDIDSLVRCMLQGRHGWQTDQYFCYQVILVLTREL 356  
QY 460 LA 461  
DB 357 QA 358

RESULT 12

US-10-177-980-12

Sequence 12, Application US/10177980

Publication No. US2003016232A1

GENERAL INFORMATION:

APPLICANT: Saraz, Jan  
APPLICANT: Franz, Petra  
APPLICANT: Aspenstrum, Pontus  
APPLICANT: Helman, Ulf  
APPLICANT: Gones, Leonel Jorge  
APPLICANT: Heldin, Carl-Henrik  
TITLE OF INVENTION: PAR6, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PIPPLI  
FILE REFERENCE: L0461/7030  
CURRENT APPLICATION NUMBER: US/10/177,980  
CURRENT FILING DATE: 2002-06-21  
PRIOR APPLICATION NUMBER: US/09/080,855  
PRIOR FILING DATE: 1998-05-18  
PRIOR APPLICATION NUMBER: 08/805,583  
PRIOR FILING DATE: 1997-02-25  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 12

LENGTH: 2466  
TYPE: PRT  
ORGANISM: Homo sapiens

US-10-177-980-12  
Query Match 26.2%; Score 639.5; DB 14; Length 2466;

Best Local Similarity 37.8%; Pred. No. 8e-49;  
Matches 137; Conservative 62; Mismatches 128; Indels 35; Gaps 6;

QY 108 PEPLSDDETFWVDVSDSLRNKNSMDESETAGPSKTVSPVLSGSSRLSKDTETVSSEKE 167  
DB 2120 PEKKTDDDEITWG-NDDELPIERTNHBDS-----KD-HSFLTNDE 2158  
QY 168 LFOAQRPLINSSARSAMDCLNTLQ-----KKEELDIREFLEBQMTLPDDENS 220  
DB 2159 LAVLPVVKVLPSCGTGANLKSIVIRLGLDQGISKELEMLQELKPLDQCL----- 2212  
QY 221 GNTLONRDKRKYDILPYDSTRVPLGKNDYINASYIRLVNHEEYFYIATOGPLPETIE 280  
DB 2213 GQTKENRRKRYKNILPYDATRVPLDGBGGINASFIKIPVKEEFVITACQGPLPTTVG 2272  
QY 281 DFMQVLNNQNVAMITREIBGVKCYSWPISL-KEPLEFHFVSVELETFHTVQYFT 339  
DB 2273 DFMQVMEQKSTVIAAMTQVEGEEKIKQRYWPNILGKTVMNSRLRLALVRMOQLKGFV 2332  
QY 340 VRVFOIVKSTGSCQCKHLOFTKPDHGTSPASADFFIKYRVYRKSHITGPLVHCSAG 399  
DB 2333 VRAMTLEDIQTREVRHISHLNFTAMPDHDTPSQPDDLTFISYMRHHSRGPITTHCSAG 2392  
QY 400 VGRGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMITQKQYQFCYEIVLEVLQNL 459  
DB 2393 IGRSGTLCIDVVLGLISQDLDFDISDLVRCKRLQHRGMVQTEDOYIFCYQVILVYLTRL 2452  
QY 460 LA 461  
DB 2453 QA 2454

## RESULT 13

US-09-802-669-46  
Sequence 46, Application US/09802669  
Patent No. US2002000490A1  
GENERAL INFORMATION:  
APPLICANT: Dean, Nicholas M.  
APPLICANT: Marcussen, Eric G.  
APPLICANT: Wyatt, Jacqueline  
APPLICANT: Zhang, Hong  
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling  
FILE REFERENCE: ISPH-545  
CURRENT APPLICATION NUMBER: US/09/802,669  
CURRENT FILING DATE: 2001-03-09  
PRIOR APPLICATION NUMBER: US 09/665,615  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: US 09/290,640  
PRIOR FILING DATE: 1999-04-12  
NUMBER OF SEQ ID NOS: 180  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 46  
LENGTH: 2485  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-802-669-46

Query Match 26.2%; Score 639.5; DB 9; Length 2485;  
Best Local Similarity 37.8%; Pred. No. 8.1e-49;  
Matches 137; Conservative 62; Mismatches 128; Indels 35; Gaps 6;

QY 108 PEPLSDDETFWVDVSDSLRNKNSMDESETAGPSKTVSPVLSGSSRLSKDTETVSSEKE 167  
DB 2139 PEKKTDDDEITWG-NDDELPIERTNHBDS-----KD-HSFLTNDE 2177  
QY 168 LFOAQRPLINSSARSAMDCLNTLQ-----KKEELDIREFLEBQMTLPDDENS 220  
DB 2178 LAVLPVVKVLPSCGTGANLKSIVIRLGLDQGISKELEMLQELKPLDQCL----- 2212  
QY 221 GNTLONRDKRKYDILPYDSTRVPLGKNDYINASYIRLVNHEEYFYIATOGPLPETIE 280  
DB 2213 GQTKENRRKRYKNILPYDATRVPLDGBGGINASFIKIPVKEEFVITACQGPLPTTVG 2291  
QY 281 DFMQVLNNQNVAMITREIBGVKCYSWPISL-KEPLEFHFVSVELETFHTVQYFT 339  
DB 2273 DFMQVMEQKSTVIAAMTQVEGEEKIKQRYWPNILGKTVMNSRLRLALVRMOQLKGFV 2332  
QY 340 VRVFOIVKSTGSCQCKHLOFTKPDHGTSPASADFFIKYRVYRKSHITGPLVHCSAG 399  
DB 2333 VRAMTLEDIQTREVRHISHLNFTAMPDHDTPSQPDDLTFISYMRHHSRGPITTHCSAG 2392  
QY 400 VGRGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMITQKQYQFCYEIVLEVLQNL 459  
DB 2393 IGRSGTLCIDVVLGLISQDLDFDISDLVRCKRLQHRGMVQTEDOYIFCYQVILVYLTRL 2452  
QY 460 LA 461  
DB 2453 QA 2454

QY 281 DFMQVLNNQNVAMITREIBGVKCYSWPISL-KEPLEFHFVSVELETFHTVQYFT 339  
DB 2292 DFMQVMEQKSTVIAAMTQVEGEEKIKQRYWPNILGKTVMNSRLRLALVRMOQLKGFV 2351  
QY 340 VRVFOIVKSTGSCQCKHLOFTKPDHGTSPASADFFIKYRVYRKSHITGPLVHCSAG 399  
DB 2352 VRAMTLEDIQTREVRHISHLNFTAMPDHDTPSQPDDLTFISYMRHHSRGPITTHCSAG 2411  
QY 400 VGRGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMITQKQYQFCYEIVLEVLQNL 459  
DB 2412 IGRSGTLCIDVVLGLISQDLDFDISDLVRCKRLQHRGMVQTEDOYIFCYQVILVYLTRL 2471  
QY 460 LA 461  
DB 2472 QA 2473

## RESULT 14

US-10-619-220-46  
Sequence 46, Application US/10619220  
Publication No. US2004003979A1  
GENERAL INFORMATION:  
APPLICANT: Dean, Nicholas M.  
APPLICANT: Marcussen, Eric G.  
APPLICANT: Wyatt, Jacqueline  
APPLICANT: Zhang, Hong  
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling  
FILE REFERENCE: ISPH-545  
CURRENT APPLICATION NUMBER: US/10/619,220  
CURRENT FILING DATE: 2003-07-14  
PRIOR APPLICATION NUMBER: 09/802,669  
PRIOR FILING DATE: 2001-03-01  
PRIOR APPLICATION NUMBER: US 09/665,615  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: US 09/290,640  
PRIOR FILING DATE: 1999-04-12  
NUMBER OF SEQ ID NOS: 180  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 46  
LENGTH: 2485  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-619-220-46

Query Match 26.2%; Score 639.5; DB 12; Length 2485;  
Best Local Similarity 37.8%; Pred. No. 8.1e-49;  
Matches 137; Conservative 62; Mismatches 128; Indels 35; Gaps 6;

QY 108 PEPLSDDETFWVDVSDSLRNKNSMDESETAGPSKTVSPVLSGSSRLSKDTETVSSEKE 167  
DB 2139 PEKKTDDDEITWG-NDDELPIERTNHBDS-----KD-HSFLTNDE 2177  
QY 168 LFOAQRPLINSSARSAMDCLNTLQ-----KKEELDIREFLEBQMTLPDDENS 220  
DB 2178 LAVLPVVKVLPSCGTGANLKSIVIRLGLDQGISKELEMLQELKPLDQCL----- 2231  
QY 221 GNTLONRDKRKYDILPYDSTRVPLGKNDYINASYIRLVNHEEYFYIATOGPLPETIE 280  
DB 2232 GQTKENRRKRYKNILPYDATRVPLDGBGGINASFIKIPVKEEFVITACQGPLPTTVG 2291  
QY 281 DFMQVLNNQNVAMITREIBGVKCYSWPISL-KEPLEFHFVSVELETFHTVQYFT 339  
DB 2292 DFMQVMEQKSTVIAAMTQVEGEEKIKQRYWPNILGKTVMNSRLRLALVRMOQLKGFV 2351  
QY 340 VRVFOIVKSTGSCQCKHLOFTKPDHGTSPASADFFIKYRVYRKSHITGPLVHCSAG 399  
DB 2352 VRAMTLEDIQTREVRHISHLNFTAMPDHDTPSQPDDLTFISYMRHHSRGPITTHCSAG 2411  
QY 400 VGRGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMITQKQYQFCYEIVLEVLQNL 459  
DB 2412 IGRSGTLCIDVVLGLISQDLDFDISDLVRCKRLQHRGMVQTEDOYIFCYQVILVYLTRL 2471  
QY 460 LA 461  
DB 2472 QA 2473



Db 2472 QA 2473

```

RESULT 15
US-10-408-765A-1349
; Sequence 1349, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Rahy, Boia D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Marnock, Dale S.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1349
; LENGTH: 2485
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1349

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Query Match 26.2%; Score 639.5; DB 16; Length 2485;  
 Best Local Similarity 37.8%; Pred. No. 8.1e-49;  
 Matches 137; Conservative 62; Mismatches 128; Indels 35; Gaps 6;

```

QY 108 PEPLESDTDEYVWVDESLNRNMSDSETPAGSKTVSPVLSGSSRLSKDTETVSSEKE 167
DB 2139 PQEKKTDDELITWG-NDELPIERTNHEBD-----KD-HSFLTND 2177
QY 168 LTOJLAQIRPFLFNSSARSARDCINTLQ-----KKEBIDIREFLEBQMTLPDDFNS 220
DB 2178 LAVLPVVKVLPSPGKYTGANLKSIVIRVLGILDQGIPSKELENTLQELKPLDQCLI----- 2231
QY 221 GNTLONDRKXRYDILPYDSTRVPLGKKKQDYINASYIRIVNHEEYFIATOGPLPETIB 280
DB 2232 GOTEKRNKRYKXILPFDATRVPLGDEGTYINASFYIKIVGKEEFYIACQGPLPTTVG 2291
QY 281 DFMQVLENNQNVITAMITREIEGVIKCYSPISL-KEPLAEHFVSVFLETFRVTQYFT 339
DB 2292 DFMQVLENNQNVITAMITREIEGVIKCYSPISL-KEPLAEHFVSVFLETFRVTQYFT 339
QY 340 VRVFOIYKSKSQCYKHLQFTKYPDHGTPASADFIKIVRYRYRKSHTITGZLVHCSAG 399
DB 2352 VRANTLSDIQRVRHSHLNFPMPHDTPSPDPDLTFITISYRHHIRSGPITTHCSAG 2411
QY 400 VGRIVFICVVDVVSALIKYSPFINNIIVTQMRKQRCAMIQTEKQYQCYEIVLEVQLNL 459
DB 2412 IGRSGTILICIDVWGLISQDLPDISLVRCMLQRHGMVQTEBDQYIFCYQVILIVLTRL 2471
QY 460 LA 461
DB 2472 QA 2473

```

Search completed: June 18, 2004, 19:46:03  
 Job time : 50 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:36:23 ; Search time 20 Seconds

(without alignments)  
2226.834 Million cell updates/sec

Title: US-09-095-478A-6

Sequence: 1 MSSEPRKRYKGTGRDNDEEG.....QYCFYELVLENTLALY 463

Scoring table: BIOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	1306	53.5	398	2	T08716
2	650	26.7	2450	2	S71625
3	639.5	26.2	2294	2	167630
4	639.5	26.2	2466	2	167629
5	631.5	25.9	2490	1	A54971
6	519	21.3	1187	1	UC4155
7	501	20.5	933	1	A41109
8	497	20.4	1189	1	UC2366
9	497	20.4	2051	2	T30938
10	488.5	20.0	597	2	B53978
11	487	20.0	926	1	A41105
12	487	20.0	1337	1	T38670
13	484.5	19.9	1175	2	S51005
14	484	19.8	1156	2	T23308
15	483	19.8	1499	2	T50212
16	481.5	19.7	1912	2	A56178
17	481	19.7	1176	2	I58345
18	477.5	19.6	1457	1	A48066
19	476	19.5	1282	1	A48758
20	476	19.5	1496	1	A48758
21	476	19.5	1501	2	I58148
22	476	19.5	1863	2	S46217
23	475	19.5	694	2	A53978
24	475	19.5	1238	2	S68700
25	474.5	19.5	1907	2	S50893
26	473.5	19.4	1997	2	S12050
27	471.5	19.3	1174	2	I38140
28	469.5	19.2	583	2	S17671
29	468.5	19.2	582	2	A57068

30	468.5	19.2	1290	2	A56493	leucocyte common a
31	468	19.2	1452	1	S17669	protein-tyrosine-p
32	468	19.2	1691	1	D54689	protein-tyrosine-p
33	468	19.2	1894	2	C54689	protein-tyrosine-p
34	467.5	19.2	387	1	A60345	protein-tyrosine-p
35	467.5	19.2	1897	1	TDHULK	leukocyte antigen-
36	467	19.1	2314	1	A46151	protein-tyrosine-p
37	466.5	19.1	415	1	A33899	protein-tyrosine-p
38	466.5	19.1	1898	2	S46216	leukocyte antigen-
39	466	19.1	377	1	A48711	protein-tyrosine-p
40	466	19.1	1452	1	S17670	protein-tyrosine-p
41	463	19.0	405	2	I49372	protein-tyrosine-p
42	462	18.9	1188	1	A57064	protein-tyrosine-p
43	462	18.9	1216	2	S60613	protein-tyrosine-p
44	461.5	18.9	1440	2	UC6312	protein-tyrosine-p
45	461	18.9	382	1	A38191	protein-tyrosine-p

#### ALIGNMENTS

##### RESULT 1

T08716

protein-tyrosine-phosphatase homolog DKFZp566K0524.1 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #ext\_change 13-Aug-1999

C/Accession: T08716

R:Anisotropy, W.; Witzner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, May 1999

A:Reference number: Z16472

A/Accession: T08716

A/Molecule type: mRNA

A/Residues: 1-398 <ANS>

A/Cross-references: EMBL:AL050040

A/Experimental source: fetal kidney; clone DKFZp566K0524

C/Genetic: A/Note: DKFZp566K0524.1

C/Superfamily: protein-tyrosine-phosphatase homology

P:161-379/Domain: protein-tyrosine-phosphatase homology <PTP>

Query Match 53.5%; Score 1306; DB 2; Length 398;

Best Local Similarity 65.8%; Pred. No. 2.4e-86;

Matches 252; Conservative 48; Mismatches 75; Indels 8; Gaps 2;

QY	81	IFGNKNSSENVKPKSHHLSRSDKYLVEPELESDDTDETWVSDSLRKNMSDSEAG	140
DB	22	VEENKYNSEKVKLSLRNPANDYEDVFESSESDPSMTARGPRRDRSSDEBEAG	81
QY	141	PKRTVSPVLSSGSRSLKDTETSVSEKELTOLAQIRPLIFNSARSAMDCLTLQKK	EE 199
DB	82	PGQALSPILS-----DTRKIVSGELDQLAQIRPLIFNFGQAIKDCILBEKTA	134
QY	200	LIITREPLEEOMTLPDDFNSGNTIOMDKRYRILPLPDSRVRPLGKKNQITNASTRI	259
DB	135	YIMQEPMALEKKNLPGERTSGNPSNRKPKRILPLPDSRVRPLGSKSKDITNASTRI	194
QY	260	VNHESEYFIATQGLPETIIBDFQWVLENNCNVAMITREIEGVIKCYSTWPISTAKP	319
DB	195	VACGEYFIATQGLPETIIBDFQWVLENNCNVAMITREIEGVIKCYSTWPISTAKP	254
QY	320	LEFHFSPVLEFHYATQYFTRAVFOIVKSKGSCQVHLOTKRPPDHGTPASADFFIKY	379
DB	255	LELKHFRVLENYQILOQYFTRAVFOIVKSKGSCQVHLOTKRPPDHGTPASADFFIKY	314
QY	380	VAYVKKSHITGPILVHCSAGVARTGVFICDVVFSAIKENYSFDIMNIVYQGRKORCGI	439
DB	315	IRYAKSHLTPGMVHVSAGIGRTGVFLCVDVVPALVYKDSFNIMDVAQMRBGRGAV	374
QY	440	QTKQYQCYTSLVLENTLAL 462	
DB	375	QTKQYHFCYDIVEVLRKLT 397	

## RESULT 2

71625  
 protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 13 - mouse  
 M:Alternate names: epidermal growth factor-binding protein; serine proteinase  
 C:Species: Mus musculus (house mouse)  
 C:Date: 27-Nov-1997 #sequence revision 12-Dec-1997 #text\_change 21-Jun-2002  
 C:Accession: S71625; S67987; I81210; I81209; S40290  
 R:Chida, D.; Kume, T.; Mukoyama, Y.; Tabata, S.; Nomura, N.; Thomas, M.L.; Matanabe, T.  
 FEBS Lett. 358, 233-239, 1995  
 A:Title: Characterization of a protein tyrosine phosphatase (RIP) expressed at a very es  
 A:Reference number: S71625; MUID:95145716; PMID:7843407  
 A:Accession: S71625  
 A:Molecule type: mRNA  
 A:Residues: 1-2450 <CH1>  
 A:Cross-references: EMBL:D83966; NID:G1232103; PIDN:BA12158.1; PID:G1232104  
 A:Experimental source: strain DBA/2; cell line MEL 745A  
 R:Wolf, B.B.; Brown, M.D.  
 FEBS Lett. 376, 177-180, 1995  
 A:Title: Epidermal growth factor-binding protein activates soluble and receptor-bound s  
 A:Reference number: S67987; MUID:96105375; PMID:7498536  
 A:Accession: S67987  
 A:Molecule type: protein  
 A:Residues: 1098-1102 <W0>  
 A:Experimental source: submaxillary glands  
 R:Sato, T.; Irie, S.; Kitada, S.; Reed, J.C.  
 Science 268, 411-415, 1995  
 A:Title: FAP-1: a protein tyrosine phosphatase that associates with Fas.  
 A:Reference number: I59595; MUID:95232528; PMID:7536343  
 A:Accession: I81210  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1329-1354, 'K', 1356-1447, 'R', 1449-1454 <RES>  
 A:Cross-references: GB:I34582; NID:G806297; PIDN:AAC42056.1; PID:G806298  
 A:Accession: I81209  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1338-1354, 'K', 1356-1447, 'R', 1449-1454 <RES>  
 A:Cross-references: GB:I34581; NID:G806295; PIDN:AAC42055.1; PID:G806296  
 R:Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Kieringa, B.  
 submitted to the EMBL Data Library, June 1993  
 A:Description: Assessment of the expression levels of murine protein-tyrosine phosphatase  
 A:Reference number: S40280  
 A:Accession: S40290  
 A:Molecule type: mRNA  
 A:Residues: 2266-2372 <HEN>  
 A:Cross-references: EMBL:Z23059; NID:G438155; PIDN:CA80594.1; PID:G438156  
 C:Genetics:  
 A:Gene: Ptpn13  
 A:Map position: 5  
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GIGF domain homology;  
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; transmembrane protein; tyros  
 F:566-860/Domain: protein 4.1 membrane-binding domain homology <B41>  
 F:1089-1165/Domain: GIGF domain homology <GLG1>  
 F:1361-1437/Domain: GIGF domain homology <GLG2>  
 F:1495-1574/Domain: GIGF domain homology <GLG3>  
 F:1769-1840/Domain: GIGF domain homology <GLG4>  
 F:1863-1937/Domain: GIGF domain homology <GLG5>  
 F:12203-2422/Domain: protein-tyrosine-phosphatase homology <PTP1>  
 F:2374/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:2380/Binding site: substrate phosphate (Arg) #status predicted

Query Match 26.7%; Score 650; DB 2; Length 2450;  
 Best local similarity 35.1%; Pred. No. 4.9e-38;  
 Matches 150; Conservative 68; Mismatches 129; Indels 80; Gaps 8;

QY 106 VPEPLSDTDETWVDSDRLRNKNSM----- 134  
 Db 2022 IYDPQAEVIGQSLDLDVDEDAQNLNQRATRAACSPDPLRTGALPESGDTIDYNSPL 2081  
 QY 135 -----DSETAGPSKTVSPVLSGSSRLSK-----DTETS-----VSR 165  
 Db 2082 PEDVPSVSSGEGKVDLASILTAASQEEKPIEDATQESRSTTETTGEDSSKOPPLTN 2141

QY 166 KEILQIAIRPLIFNSSARSAKDCLNTQ-----KKEELDIREFLEBQMTLPDPR 218  
 Db 2142 BELAALFVAVPPSGKTTGTQLOQNTITRLDGLDQIPSELEMLDGLKPLDCLT--- 2197  
 QY 219 NSGNTLQNRDNKNRYRDLIPYDSTRVPLGKNKQDYNASYIRIVNHEEYFIATQGPLPET 278  
 Db 2198 --GQTKENRRKKNRYKNILPDTTRVPLGDEGYNATFIRIPVGTQFVYIACGGLPFT 2255  
 QY 279 IEPQWVLENNQNVNLTIRETECGVVKQSYWPISTL-KEPLFEHFSVPLEFHTQY 337  
 Db 2256 VSPDWQVWQNSTVLAQMTQVEGEEKIKQRYWPSITIGTTVANEERLRLALRMOQLKG 2315  
 QY 338 FTVRFOIVKSTGSKQCVKHLQFTKWPDHGTBASAD---FFIKRYVYVYKSHITGELV 394  
 Db 2216 FIVRVALLIEDIQGEVYHSHLAFWMPDHDTSGPDLLTFISYWRHRRS---GPVIT 2372  
 QY 395 HGSAGVGRVTFICVDVYSAIRKNTSPDLMIVTQMRQRCGMQCTKQCYCYEIVLE 454  
 Db 2373 HGSAGVGRSGTLCTIDVIGALISQDLFDISLVRCLRQRMQVQTEGQVFCYQVITLY 2432  
 QY 455 VLAQNLTA 461  
 Db 2433 VLTHTLQA 2439

## RESULT 3

167630  
 protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 3 -  
 C:Species: Homo sapiens (man)  
 C:Date: 29-May-1998 #sequence revision 29-May-1998 #text\_change 30-Jun-2002  
 C:Accession: I67630  
 R:Meekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.  
 FEBS Lett. 337, 200-206, 1994  
 A:Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membran  
 A:Reference number: I53483; MUID:94116679; PMID:8287977  
 A:Accession: I67630  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-2294 <RES>  
 A:Cross-references: GB:D21211; NID:G452193; PIDN:BA04752.1; PID:G452194  
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GIGF domain homology;  
 C:Keywords: phosphoric monoester hydrolase  
 F:574-868/Domain: protein 4.1 membrane-binding domain homology <B41>  
 F:1182-1258/Domain: GIGF domain homology <GLG2>  
 F:2046-2265/Domain: protein-tyrosine-phosphatase homology <PTP>

Query Match 26.2%; Score 639.5; DB 2; Length 2294;  
 Best local similarity 37.8%; Pred. No. 2.5e-37;  
 Matches 137; Conservative 62; Mismatches 128; Indels 35; Gaps 6;

QY 108 PEPLSDTDETWVDSDRLRNKNSMDSBTAGPSKTVSPVLSGSSRLSDTETSVEKE 167  
 Db 1948 PQKKTIDDEBITWG-NDELPKERTHEDSD-----KD-HSFITNDE 1986  
 QY 168 LTQLAQIRPLIFNSSARSAKDCLNTQ-----KKEELDIREFLEBQMTLPDPRNS 220  
 Db 1987 LALVPAVKVLPSGKYKGMKSVIRVRLQGLDQIPSKLEMLQELKPLDQCLT----- 2040  
 QY 221 GNTLQNRDNKNRYRDLIPYDSTRVPLGKNKQDYNASYIRIVNHEEYFIATQGPLPET 280  
 Db 2041 GQTKENRRKKNRYKNILPDTTRVPLGDEGYNATFIRIPVGTQFVYIACGGLPFTTG 2100  
 QY 281 DFWQVLENNQNVNLTIRETECGVVKQSYWPISTL-KEPLFEHFSVPLEFHTQY 339  
 Db 2101 DFWQVLENNQNVNLTIRETECGVVKQSYWPISTL-KEPLFEHFSVPLEFHTQY 339  
 QY 340 VAVFOIVKSTGSKQCVKHLQFTKWPDHGTBASADFFIKRYVYVYKSHITGELVCSG 399  
 Db 2161 VAVFOIVKSTGSKQCVKHLQFTKWPDHGTBASADFFIKRYVYVYKSHITGELVCSG 399  
 QY 400 VAVFOIVKSTGSKQCVKHLQFTKWPDHGTBASADFFIKRYVYVYKSHITGELVCSG 459  
 Db 2221 IGRSGTLCIDVIGALISQDLFDISLVRCLRQRMQVQTEGQVFCYQVITLY 2280

QY 460 LA 461  
Db 2281 QA 2282

RESULT 4  
167629  
protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 2 -  
C:Species: Homo sapiens (man)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 30-Jun-2002  
C:Accession: 167629  
R:Maekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.  
FEBS Lett. 337, 200-206, 1994  
A:Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane  
A:Reference number: 153483; MUID:94116679; PMID:8287977  
A:Accession: 167629  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-2466 <RES>  
A:Cross-references: GB:D21210; NID:9452191; PIDN:BA04751.1; PID:9452192  
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;  
C:Keywords: phosphoric monoester hydrolase  
F:574-868/Domain: protein 4.1 membrane-binding domain homology <B41>  
F:1354-1430/Domain: GLGF domain homology <GLG2>  
F:1218-2437/Domain: protein-tyrosine-phosphatase homology <PTP>

Query Match 26.2%; Score 639.5; DB 2; Length 2466;  
Best Local Similarity 37.8%; Pred. No. 2.8e-37;  
Matches 137; Conservative 62; Mismatches 128; Indels 35; Gaps 6;

QY 108 PEPLESDVDETVWDVDRSLRNRNMSDSETAGSKTVSPVLSGSSRLSKDTTSVEKE 167  
Db 2120 PSEKTDDEITWG-NDELPRIERTNHESD-----KD-HSFLTND 2158  
QY 168 LTQLAQIRPLIFNSSASASAMDCINTLQ-----KKEELDIREFLEQMTLPDDFNS 220  
Db 2159 LAVLPVYKVLPSGKYTGAMLSKSVIRLRLGLDQGIPEKLEMLQELKPLDQCL 2212  
QY 221 GNTLQNRDKRRDILPDTSTRVPLGKNDYINASTYIRIVNHEEYFYATGSPLETTIE 280  
Db 2213 GQTKENRRKRRYKNILPYDARVPLDGEQYINASTYIRIVNHEEYFYATGSPLETTIE 2272  
QY 281 DFMQWLENNCNVAMITREIECGVTKCYSPYPIST-KEPLEFHSVLETFHVYQYFT 339  
Db 2273 DFMQWLENNCNVAMITREIECGVTKCYSPYPIST-KEPLEFHSVLETFHVYQYFT 2332  
QY 340 VRFQIVKSTGSKQCVKHLQFTKMPDHGTPASADPFIKYRVYRKSHITGPIVHCSAG 399  
Db 2233 VRFQIVKSTGSKQCVKHLQFTKMPDHGTPASADPFIKYRVYRKSHITGPIVHCSAG 2392  
QY 400 VGRGVFICVDVVFSALEKNVSPDMNITVQKRCRCGILQKQGFCEYEVLEVLQNL 459  
Db 2293 VGRGVFICVDVVFSALEKNVSPDMNITVQKRCRCGILQKQGFCEYEVLEVLQNL 2452  
QY 460 LA 461  
Db 2453 QA 2454

RESULT 5  
A54971  
protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 1 (Y  
N:Alternate names: Fas-associated phosphatase FAP-1; protein-tyrosine-phosphatase hPTP1E  
C:Species: Homo sapiens (man)  
C:Date: 11-Nov-1994 #sequence\_revision 08-Feb-1996 #text\_change 21-Jun-2002  
C:Accession: A54971; A55114; I59595; I53483; S46955  
R:Banville, D.; Ahmad, S.; Stocco, R.; Shen, S.H.  
J. Biol. Chem. 269, 22320-22327, 1994  
A:Title: A novel protein-tyrosine phosphatase with homology to both the cytoskeletal pro  
A:Reference number: A54971; MUID:94350988; PMID:8071359  
A:Accession: A54971  
A:Molecule type: mRNA

A:Residues: 1-2490 <BAN>  
A:Cross-references: GB:U12128  
A:Note: sequence shown follows authors' translation at positions 62-63  
R:Saras, U.; Claesson-Welsh, L.; Heldin, C.H.; Gonsky, L.V.  
J. Biol. Chem. 269, 24082-24089, 1994  
A:Title: Cloning and characterization of PTP1E, a protein tyrosine phosphatase with six  
A:Reference number: A55114; MUID:95014139; PMID:7929060  
A:Accession: A55114  
A:Molecule type: mRNA  
A:Residues: 1-61, 'GS', 64-839, 'D', 841-1055, 1075-1133, 'FH', 1136-1210, 'I', 1212-1383, 1389-1  
A:Cross-references: GB:X80289; NID:9515030; PIDN:CA45653.1; PID:9515031  
R:Sato, T.; Irie, S.; Kitada, S.; Reed, D.C.  
Science 268, 411-415, 1995  
A:Title: FAP-1, a protein tyrosine phosphatase that associates with Fas.  
A:Reference number: I59595; MUID:95232528; PMID:7556333  
A:Accession: I59595  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1279-1888 <RES>  
A:Cross-references: GB:L34583; NID:9806291; PIDN:AA41755.1; PID:9806292  
R:Maekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.  
FEBS Lett. 337, 200-206, 1994  
A:Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membran  
A:Reference number: 153483; MUID:94116679; PMID:8287977  
A:Accession: 153483  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-61, 'GS', 64-839, 'D', 841-1210, 'I', 1212-1383, 1389-2299, 'QM', 2302-2490 <RES>  
A:Cross-references: GB:D21209; NID:9452189; PIDN:BA04750.1; PID:9452190  
C:Genetic:  
A:Gene: GDB:PTPN13  
A:Map position: 4q21.3-q21.3  
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;  
C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyros  
F:574-868/Domain: protein 4.1 membrane-binding domain homology <B41>  
F:1099-1175/Domain: GLGF domain homology <GLG1>  
F:1173-1454/Domain: GLGF domain homology <GLG2>  
F:1511-1590/Domain: GLGF domain homology <GLG3>  
F:1799-1870/Domain: GLGF domain homology <GLG4>  
F:1893-1961/Domain: GLGF domain homology <GLG5>  
F:2242-2461/Domain: protein-tyrosine-phosphatase homology <PTP>  
F:2413/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:2419/Binding site: substrate phosphate (Arg) #status predicted

Query Match 25.8%; Score 631.5; DB 1; Length 2490;  
Best Local Similarity 37.3%; Pred. No. 1.1e-36;  
Matches 135; Conservative 64; Mismatches 128; Indels 35; Gaps 6;

QY 108 PEPLESDVDETVWDVDRSLRNRNMSDSETAGSKTVSPVLSGSSRLSKDTTSVEKE 167  
Db 2144 PSEKTDDEITWG-NDELPRIERTNHESD-----KD-HSFLTND 2182  
QY 168 LTQLAQIRPLIFNSSASASAMDCINTLQ-----KKEELDIREFLEQMTLPDDFNS 220  
Db 2183 LAVLPVYKVLPSGKYTGAMLSKSVIRLRLGLDQGIPEKLEMLQELKPLDQCL 2236  
QY 221 GNTLQNRDKRRDILPDTSTRVPLGKNDYINASTYIRIVNHEEYFYATGSPLETTIE 280  
Db 2237 GQTKENRRKRRYKNILPYDARVPLDGEQYINASTYIRIVNHEEYFYATGSPLETTIE 2296  
QY 281 DFMQWLENNCNVAMITREIECGVTKCYSPYPIST-KEPLEFHSVLETFHVYQYFT 339  
Db 2273 DFMQWLENNCNVAMITREIECGVTKCYSPYPIST-KEPLEFHSVLETFHVYQYFT 2336  
QY 340 VRFQIVKSTGSKQCVKHLQFTKMPDHGTPASADPFIKYRVYRKSHITGPIVHCSAG 399  
Db 2233 VRFQIVKSTGSKQCVKHLQFTKMPDHGTPASADPFIKYRVYRKSHITGPIVHCSAG 2392  
QY 400 VGRGVFICVDVVFSALEKNVSPDMNITVQKRCRCGILQKQGFCEYEVLEVLQNL 459  
Db 2293 VGRGVFICVDVVFSALEKNVSPDMNITVQKRCRCGILQKQGFCEYEVLEVLQNL 2452  
QY 460 LA 461  
Db 2417 QA 2418

Qy 460 LA 461  
Db 2477 QA 2478

## RESULT 6

UC4155  
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 14 - human  
N:Alternate names: PE2 protein; protein-tyrosine-phosphatase/ezrin-like protein  
C:Species: Homo sapiens (man)  
C:Date: 27-Aug-1995 #sequence\_revision 23-Feb-1996 #text\_change 21-Jul-2000  
C:Accession: UC4155  
R:Smith, A., Mitchell, P.J., Shibley, J., Gusterson, B.A., Rogers, M.V., Crompton, M.R.  
Biochem. Biophys. Res. Commun. 209, 959-965, 1995  
A:Title: PE2, a novel human cDNA encoding protein tyrosine phosphatase and ezrin-like dom  
A:Reference number: UC4155; MIM:95251727; PMID:7733990  
A:Accession: UC4155  
A:Molecule type: mRNA  
A:Residues: 1-1187 <SMIT>  
A:Cross-references: EMBL:X82676; NID:G3929753; PIDN:CAA57993.1; PID:G809029  
A:Experimental source: breast  
C:Genetics:  
A:Gene: GDB:PTPN14  
A:Cross-references: GDB:454485  
A:Map position: 1q32.2-q32.2  
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-b  
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase  
F:23-302/Domain: protein 4.1 membrane-binding domain homology <B41>  
F:566-575/Region: proline-rich  
F:709-716/Region: acidic  
F:933-1169/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F:1121/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1127/Binding site: substrate phosphate (Arg) #status predicted

Query Match 21.3%; Score 519; DB 1; Length 1187;  
Best Local Similarity 32.0%; Pred. No. 4.5e-29;  
Matches 143; Conservative 65; Mismatches 129; Indels 110; Gaps 14;  
Qy 107 YPELESCTBTVDVDSRSLRNKRNMSDSELA---GPSKTVS-----PVLSSGS 153  
Db 752 YPGRRKS-----VSNGLRQDQASLPAMARARVLRHGPAPAKAISMSTRDPANVAGAS 803  
Qy 154 ---RLSKDQETSVSEK-----ELTQL-----AQIR 175  
Db 804 LGPISSEPDLSVKEKRYKPEVSEKPYSEMSFLEDSIIEREMIRLEKQKAGLEQKR 863  
Qy 176 PLIFNS-----SARSADCLNTIQK-ERIDITRELEBQMTLPD 216  
Db 864 PLMLAALNGLSVAESVSGRENRVDATVPEDEFRRLKLESGMVFTEYEQIPCKKANG 923  
Qy 217 DFNSGNTLQNRDKRNYRDLPYDSTRVPL-----GKNQDYINASYIRIVNHEEYFIATQ 272  
Db 924 IFSPALPBNABERSRIRIEVPEENRVELPTKENNTGYINASHIKYVGGAMHIYATQ 993  
Qy 273 GPLPETIEDFWQVLENNCNVIAITREIECGVIKCYSTYPISLKEPLEEHSVLETF 332  
Db 984 GPLPHTCHDWMQWMEQGVAVIAVYTAEEGGRKSRHYP-----KLGSKHSATYVGRK 1038  
Qy 333 HVTQYFTVRFQVLYKST-----GKSCVGHLOFTKMPDHGFPASADPFIKY 379  
Db 1039 KVTITKE--RTDSVCYATITGLKVKHLLSGQRITVHLOITMPPHGCHEVQSLTLEEL 1096  
Qy 380 --VAVYKSHITG-----PLVHCSAGVGRGTGVCVDVPSAIEKNYSFDIMNITVM 431  
Db 1097 QVSRHNTSMLEGGKXNHRPIVWCHSAGVGRGTGLILSBIMLYCLEHNEKEVPMMLRL 1156  
Qy 432 RKQRCGMIOFKBOYOPCYEIVLEVLON 458  
Db 1157 RQGRMEIQTIIAQIKFYVQVLIQFLQN 1183

## RESULT 7

A41109

protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN3, nonreceptor type 3 [validated] - huma

N:Alternate names: PTPN3  
C:Species: Homo sapiens (man)  
C:Date: 27-Mar-1992 #sequence\_revision 02-May-1994 #text\_change 21-Jun-2002  
C:Accession: A41109; I55698  
R:Yang, Q., Tonks, N.K.  
Proc. Natl. Acad. Sci. U.S.A. 88, 5949-5953, 1991  
A:Title: Isolation of a cDNA clone encoding a human protein-tyrosine phosphatase with h  
A:Reference number: A41109; MIM:9126738; PMID:1648725  
A:Accession: A41109  
A:Molecule type: mRNA  
A:Residues: 1-913 <YAN>  
A:Cross-references: GB:M64572; NID:g179912; PIDN:AAA35647.1; PID:g179913  
R:Ikuta, S., Itoh, F., Honda, Y., Toyota, M., Makiuchi, Y., Imai, K., Yachi, A.  
J. Gastroenterol. 29, 727-732, 1994  
A:Title: Expression of cytoskeletal-associated protein tyrosine phosphatase PTPN3 mRNA  
A:Reference number: I55698; MIM:95179278; PMID:7674267  
A:Accession: I55698  
A:Status: Translated from GB/EMBL/DBJ  
A:Residues: 899-913 <RBS>  
A:Molecule type: mRNA  
A:Cross-references: GB:S76309; NID:g913165; PIDN:AAB33583.1; PID:g913166  
C:Genetics:  
A:Gene: GDB:PTPN3  
A:Cross-references: GDB:131386; OMIM:176877  
A:Map position: 9q31-q31  
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 3; GIGF domain homology;  
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase  
F:31-308/Domain: protein 4.1 membrane-binding domain homology <B41>  
F:516-590/Domain: GIGF domain homology <GIG>  
F:670-890/Domain: protein-tyrosine-phosphatase homology <PTP>  
F:882/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:882/Binding site: substrate phosphate (Arg) #status predicted

Query Match 20.5%; Score 501; DB 1; Length 913;  
Best Local Similarity 37.4%; Pred. No. 6e-29;  
Matches 119; Conservative 44; Mismatches 110; Indels 45; Gaps 10;  
Qy 164 SEKELTQALQIRPLINSSASARNDCI--NTLQKKBIDITREPLEEQM----- 212  
Db 607 SEDELNQL--FPAIFPMCPBEG--DTLEGSNAOLKKGESGTVLLQFQELRYKKDELAI 662  
Qy 213 ---TLPPDNGNTLQNRDKRNYRDLPYDSTRVPLGKQKQDYINASYI-----RIYVH 262  
Db 663 TRAKLP-----QNDKRNKYQVLEPYDTRRVLLQGMEDITNSYAMETPAALVAK 713  
Qy 263 EEEYFIATQGPLPETIEDFWQVLENNCNVIAITREIECGVIKCYSTYPISLKEPLEF 322  
Db 714 ---YIATQGLPHTCAQFMQVWVDQKSLIVMLTTLERGRTRCHQYWP---DPPDVH 765  
Qy 323 EH--FSVLETFHVTQYFTVRFQVLYKSTGKSCVGHLOFTKMPDHGFPASADPFIKY 380  
Db 766 NNGGHIOQCSHDCITAYSRKMLVNTQTGSEHTVTHLQYAMPDHGIPDDSSDFLEEV 825  
Qy 381 RYVRKSHI--TGPLVHCSAGVGRGTGVCVDVPSAIEKNYSFDIMNITVMKRCQKGI 439  
Db 826 NYVRSIRLVDSBVLVHCSAGIGRTGLVLTETPACLTETRNLPYELDIYRKGRDQRAKAY 885  
Qy 440 QTKBOYOPCYEIVLEVLQ 457  
Db 886 QTSQKIFVCEALIRVYS 903

## RESULT 8

UC3366  
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 14 - mouse  
N:Alternate names: PE2 protein; protein-tyrosine-phosphatase PTP36; protein-tyrosine-ph  
C:Species: Mus musculus (house mouse)  
C:Date: 24-Feb-1995 #sequence\_revision 23-Feb-1996 #text\_change 21-Jul-2000  
C:Accession: UC3366  
R:Sawada, M., Ogata, M., Fujino, Y., Hamaoka, T.  
Biochem. Biophys. Res. Commun. 203, 479-484, 1994  
A:Title: cDNA cloning of a novel protein tyrosine phosphatase with homology to cytoskel

A:Reference number: JC2366; MUID:94354845; PMID:8074693  
 A:Accession: JC2366  
 A:Molecule type: mRNA  
 A:Residues: 1-1189 <SW>  
 A:Cross-references: GB:D31842; NID:G507330; PIDN:BA06628.1; PID:G507331  
 A:Experimental source: thymus  
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-F  
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase  
 F:23302/Domain: protein 4.1 membrane-binding domain homology <B41>  
 F:56-575/Region: proline-rich  
 F:712-718/Region: acidic  
 F:935-1171/Domain: protein-tyrosine-phosphatase homology <PTP>  
 F:1123/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:1129/Binding site: substrate phosphate (Arg) #status predicted

Query Match 20.4%; Score 497; DB 1; Length 1189;  
 Best Local Similarity 32.4%; Pred. No. 1.7e-27;  
 Matches 128; Conservative 64; Mismatches 125; Indels 78; Gaps 11;

QY 133 SMDSETPGSKTVSPVLSGSRSLSD-----TETVSSEKELT----- 169  
 DB 800 AVNGASLSPSISEPDLTSVKRVRKKEPKRPEVSEMSLEDSITEREMIRNLEKQKCTG 859  
 QY 170 QLAQIRPLIF-----NSSARSAMDCLNTLQKKELDIIRFELRQ 211  
 DB 860 POAQRPLMTALNGLSVARVSGREDGSHDTRFVIDERLRLAKKLEDGV--FTEYEQ 917  
 QY 212 MTLDD-----FNGNTLQNRDKRYDILPYDSTRPL-----GKNDYINASTIRVNH 262  
 DB 918 --IENKANGVFSTALPENASRIRREVEEENREVELLPTKENNGVYNASHIKVVG 975  
 QY 263 EEEFYIATQGLPETIEDFQWMLNENNVAMITREIEGVKICSYPISEKPLEF 322  
 DB 976 GSEHYIATQGLPETIEDFQWMLNENNVAMITREIEGVKICSYPISEKPLEF 322  
 QY 323 EHSVFLETHVQYF-----TVRFQIVKSTGSCQVKEHLOFTKPDHGTPLASADF 375  
 DB 1031 KHSSATYGVKRVKVTFTDSQCAVTGLKYNHLLSGQERTVMHLYQTDWPHHGFEDVQ 1090  
 QY 375 FIKY-----VRYVRKSHNG-----PLVHCSAGVGRGVPCVAVSATEKNSFD 423  
 DB 1091 FLSLEIEQSVKRTNVLSEIRKRPPIVHCSAGVGRGVVLSLMLTCLEHNEKVE 1150  
 QY 424 INNIWTKRQRCMIGTKEQYQCYEIVLEVLN 458  
 DB 1151 VPTMLRFLREQRMFIQITIAQKRVYQVLQNL 1185

RESULT 9  
 T30938  
 receptor tyrosine phosphatase - medicinal leech  
 C:Species: Hirudo medicinalis (medicinal leech)  
 C>Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 31-Jan-2000  
 C:Accession: T30938  
 R:Gerston, T.R.; Baker, M.; Nitebach, M.; Wu, P.; Macagno, E.R.  
 submitted to the EMBL Data Library, December 1997  
 A:Description: Two receptor tyrosine phosphatases of the LAR subfamily are expressed in  
 A:Reference number: Z20939  
 A:Accession: T30938  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-2051 <GER>  
 A:Cross-references: EMBL:AF017083; NID:G2695654; PID:G2695655; PIDN:AA091460.1  
 C:Genetics:  
 A:Gene: LAR2  
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
 ogy

Query Match 20.4%; Score 497; DB 2; Length 2051;  
 Best Local Similarity 40.3%; Pred. No. 3.8e-27;  
 Matches 106; Conservative 46; Mismatches 95; Indels 16; Gaps 7;  
 QY 205 EFLELEQ-MTLPPDPSNGNTLQNRDKRYRDLIPYDSTRVPLG-----KKQYINASTIR 258

DB 1786 EFKLSSGKTSLSFASANISCKRKRNVNVAPEYETTRVCLQPIRGVDSGDYINASFID 1845  
 QY 259 IWNHEEYFIATQGLPETIEDFQWMLNENNVAMITREIEGVKICSYPISEK 318  
 DB 1846 --GRRYRAVIAIATQGLPETIEDFQWMLNENNVAMITREIEGVKICSYPISEK 318  
 QY 319 PLEHEHRSVF-LSTEHVQYFTVRVQIVKSTGSCQVHLOFTKMPDHGTPLASADFPI 377  
 DB 1902 SARYQYFVVDPLAEYNNPQYI-LRPFVVDARQGSRTKQFQITDMPGCVSTGDPFI 1960  
 QY 378 KYRVYVRKSH-----INGPLVHCSAGVGRGVPCVAVSATEKNSFDINNIWTKR 433  
 DB 1961 DFIGQTHKTKGQSGRPVHCSAGVGRGVITLISIVLRKRFSGAVDVPTQVNLRT 2020  
 QY 434 QRCMTQTKQYQCYEIVLEVL 456  
 DB 2021 QRPQWQTEHQVAFYRAALEYL 2043

RESULT 10  
 B53978  
 protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type PTPX10 - African clawed fr  
 C:Species: Xenopus laevis (African clawed frog)  
 C>Date: 25-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 22-Jun-1999  
 C:Accession: B53978  
 R:Del Vecchio, R.L.; Tonks, N.K.  
 J. Biol. Chem. 269, 19639-19645, 1994  
 A:Title: Characterization of two structurally related Xenopus laevis protein tyrosine p  
 A:Reference number: A53978; MUID:94308257; PMID:8034733  
 A:Accession: B53978  
 A:Molecule type: mRNA  
 A:Status: preliminary  
 A:Residues: 1597 <DEL>  
 A:Cross-references: GB:B33099; NID:G495671; PIDN:AA21728.1; PID:G495672  
 A:Experimental source: ovary  
 A:Note: sequence extracted from NCBI backbone (NCBIN:149759, NCBI:P149760)  
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 9; cellular retinoidhyde  
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphat  
 F:38-227/Domain: cellular retinoidhyde-binding protein homology <CRB>  
 F:328-564/Domain: protein-tyrosine-phosphatase homology <PTP>  
 F:516/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:522/Binding site: substrate phosphate (Arg) #status predicted

Query Match 20.0%; Score 488.5; DB 2; Length 597;  
 Best Local Similarity 28.6%; Pred. No. 2.6e-27;  
 Matches 130; Conservative 76; Mismatches 164; Indels 85; Gaps 13;

QY 48 NIKYTEHLDILMVFLLITWYN---VFKL-----KKELFGNKNSENNKPS-- 94  
 DB 163 NIKKAFPARLKCVPVSSPLWFRAPFAVLRIFVEKLRERVTVANHLVNHIPRESKP 222  
 QY 95 HHLSPDKYELVYPRLESDTDRTW---DVSDELRLRNWNSMD-----SETGSPSKT 144  
 DB 223 EHLGTSKTSRV-----AMIOSCVNSKQTEQKGDCHDHPMYASQNPXSP 270  
 QY 145 VSPVLSGSSRLSKDETYSERELTQLQIRLIFNSSARSAMDCLNTLQKKELDIIR 204  
 DB 271 LPPGMELSLHMPEDGGMY-----LDLVGVKVMKKKGIRQ 306  
 QY 205 EFLELEQMTLPPDPSNGNTLQNRDKRYRDLIPYDSTRVPLG-----KKQYINASTIR 259  
 DB 307 EYEBIRKPPVSPISKSHNQVKNRSDVLCIDQSRKGLGVGTDTDTIDYINAFMD- 365  
 QY 260 VNHHEEYFIATQGLPETIEDFQWMLNENNVAMITREIEGVKICSYPISEK 319  
 DB 366 -GYKKNAYIATQGLPETIEDFQWMLNENNVAMITREIEGVKICSYPISEK 319  
 QY 320 LAFEHRSVFLERFNT--QYTVRVQIVKSTGSCQVHLOFTKMPDHGTPLASADFPI 377  
 DB 425 EDTGHP--IIRNIHIDLFQDFLTIRFVYNNQTDSESRVAHYQVSWDPFGVPKASAMT 482  
 QY 378 KYRVYVRK-----SHITG--PLVHCSAGVGRGVPCVAVSATEKNSFD 422

Db 483 DFRQVQKHQAVAVNVLQMEWTGHPAGPPIVHSCAGIGRTGTCITDICTSLRLEDIGTV 542  
 QY 423 DINNIIVTQMRKQRCGMITKEQYCFYEVLEVIQ 457  
 Db 543 DVLQTVKMRQASISITQWQYFICWAIIEVQ 577

## RESULT 11

A41105  
 Protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN4, nonreceptor type 4 [validated] - human  
 N/Alternate names: PTPase MEG  
 C/Species: Homo sapiens (man)  
 C/Date: 20-Mar-1992 #sequence\_revision 02-May-1994 #text\_change 21-Jun-2002  
 C/Accession: A41105  
 R/Gu. M.; York, J.D.; Marshawsky, I.; Majerus, P.W.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 5867-5871, 1991  
 A/Title: Identification, cloning, and expression of a cytosolic megakaryocyte protein-ty  
 A/Reference number: A41105; MUID:91288564; PMID:1648233  
 A/Accession: A41105  
 A/Molecule type: mRNA  
 A/Residues: 1-926 <GDU>  
 A/Cross-references: GB:M68941; NID:G190747; PIDN:AAA6530.1; PID:G190748  
 A/Experimental source: megakaryocytes, cell line MEG-10  
 C/Genetics:  
 A/Gene: GDB:PTPN4  
 A/Cross-references: GDB:131387; OMIM:176878  
 A/Map position: 9q31-q31  
 C/Superfamily: protein-tyrosine-phosphatase, nonreceptor type 3; GUGF domain homology; P  
 C/Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase  
 F/31-308/Domain: protein 4.1 membrane-binding domain homology <841>  
 F/523-597/Domain: GUGF domain homology <GUG>  
 F/679-900/Domain: protein-tyrosine-phosphatase homology <PTP>  
 F/852/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F/858/Binding site: substrate phosphate (Arg) #status predicted

Query Match 20.0%; Score 487; DB 1; Length 926;  
 Best Local Similarity 28.9%; Pred. No. 6.2e-27;

Matches 137; Conservative 74; Mismatches 173; Indels 90; Gaps 13;

QY 24 NLNIRNLSSSCMTPTKPVQNKTL-----MKYEH-----LDILMPLILITW 69  
 Db 490 HINFTPISSPEKPTNGGPHNLVIRKRPENGRFGFNKGYDQKRPVTSRVAR 549  
 QY 70 YNFKLWKGLIFSNK---KNSENVKPSHLSFSDKTELVPPLSDTDE-----T 118  
 Db 550 GTPADLCVPRNBSGDQVVLNGRDIAEHTH----DQVVLPTKSCHEHSELMILVRPN 605  
 QY 119 YMDVSDSLRRKRNMSSEFNGPSTVPSLSSSRSLKDTETSVSEKELTQLAQRPL 178  
 Db 606 VYDVEEKLKLN-----EPDQYIPEKAPLD 630  
 QY 179 FNSARSARMDCLNTLQKEEL---DIREFLEQMTLPDDFNSGNTLQNRKRRYDI 235  
 Db 631 SVHGDHSLRSM--IQLEGLICGYLTQFDQYRKKGPMMSCATLPRNISKRRYDI 668  
 QY 236 LPYDSTVPGLKRDYINASTYR-----IVNEEYFIATQGLPETIEDFWQVLE 288  
 Db 689 SPYDQTEVILLKGNEDYINANNIPEISSSLINO-----YIACQGLPEHTCTPFWQVLE 743  
 QY 289 NNGCIVMITREICGVYKCYVWPISLKEPLEPHEHVSLEFTHVQYTVAVFO---I 345  
 Db 744 QGSSMVMTLTQVGRGVKCHQVPE---EPYSSSTGCVYQVTHCHSEGNVAVIFRMTL 799  
 QY 346 VKKSTGSCVXKHLQFTKPDHGTSPASADFFIKYRVYRSHI--TGPLLVHCSAGVGT 403  
 Db 800 FNRKNSRPLTQIQYIAMPDHGVDDSDFLDFVCHVRNKRAGKEPVPVYHCSAGIGRT 859  
 QY 404 GVPLICVAVSAIEKKNYSFDIMNVYQMRKQRCGMITKEQYCFYEVLEVIQ 457  
 Db 860 GVLITMETANCLIECNQVPVPLDVTNRKQRAMTITPSQYRVCALIKVTE 913

## RESULT 12

I38670

Protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type J precursor - human

N/Alternate names: density enhanced phosphatase-1 (DEP-1); protein-tyrosine phosphatase

C/Species: Homo sapiens (man)

C/Date: 01-Mar-1996 #sequence\_revision 08-Mar-1996 #text\_change 22-Jun-1999

C/Accession: I38670; 152599

R/Ostman, A.; Yang, Q.; Tonks, N.K.  
 Proc. Natl. Acad. Sci. U.S.A. 91, 9680-9684, 1994

A/Title: Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase, is enhanced

A/Reference number: I38670; MUID:95024024; PMID:7937872

A/Accession: I38670

A/Molecule type: mRNA

A/Residues: 1-1337 <RES>

A/Cross-references: EMBL:U10886; NID:G558754; PID:G558755

A/Experimental source: HeLa cells

R/Honda, H.; Inazawa, J.; Nishida, J.; Yazaki, Y.; Hirai, H.  
 Blood 84, 4186-4194, 1994

A/Title: Molecular cloning, characterization, and chromosomal localization of a novel p

A/Reference number: I52599; MUID:95086212; PMID:7994032

A/Accession: I52599

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-216, 'LTVGRKA', 225-260, 'G', 262-285, 'GTGGLDASVTSRRA', 302, 'S', 304, 'TAPVHD

A/Cross-references: GB:D37781; NID:G633072; PIDN:BA07035.1; PID:G633073

C/Comment: Enhanced expression of this protein with increasing cell density suggests a

C/Genetics:  
 A/Gene: GDB:PTPNJ  
 A/Cross-references: GDB:385040; OMIM:600925

A/Map position: 19q13.4-19q13.4

C/Function:  
 A/Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine an

C/Superfamily: protein-tyrosine-phosphatase, receptor type J; fibronectin type III repe

C/Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; receptor; tra

F/1-35/Domain: signal sequence #status predicted <SIG>

F/36-1337/Domain: protein-tyrosine-phosphatase, receptor type J #status predicted <MAT

F/118-197/Domain: fibronectin type III repeat homology <3FNA>

F/206-283/Domain: fibronectin type III repeat homology <3FNA>

F/284-356/Domain: fibronectin type III repeat homology #status atypical <3FNC>

F/365-445/Domain: fibronectin type III repeat homology <3FND>

F/453-530/Domain: fibronectin type III repeat homology <3FND>

F/539-617/Domain: fibronectin type III repeat homology <3FND>

F/720-804/Domain: fibronectin type III repeat homology <3FND>

F/972-988/Domain: transmembrane #status predicted <TMN>

F/1065-1287/Domain: protein-tyrosine-phosphatase homology <PTP>

F/1287-82,99,104,142,172,231,258,278,342,351,376,391,396,413,431,501,525,536,582,603,6

F/1239/Active site: Cys (phosphocysteine intermediate) #status predicted

F/1245/Binding site: substrate phosphate (Arg) #status predicted

Query Match 20.0%; Score 487; DB 1; Length 1337;  
 Best Local Similarity 34.9%; Pred. No. 1.1e-26;

Matches 110; Conservative 63; Mismatches 114; Indels 28; Gaps 8;

QY 156 SKDTENSVEKELTQLAQRPLIFNSARSARMDCLNTQKEED---IIRPLELEQ 211  
 Db 1003 AKKNVYSFS-----QTKP---KSKLLIVENPBAVFKQQSDNSGCAEEYDNLTL 1050  
 QY 212 MTLPPDENSGNTLQNRKRRYDILPYDSTRVPLG---KNQDYINASTYRIVNHEBYE 267  
 Db 1051 VGISQPKVAAELAKRGNRRYNNVLPYDISRKLSVQTHSTDDYINANNMPGYSKDD-- 1108  
 QY 268 YIATQGLPETIEDFWQVLENNQNVAMITREICGVYKCYSPISLKEPLEHREBY 327  
 Db 1109 FIATQGLPETIEDFWQVLENNQNVAMITREICGVYKCYSPISLKEPLEHREBY 327  
 QY 328 PLETHVTVQYFTVAVFOIYKSTGSKQVXKHLQFTKPDHGTSPASADFFIKY 383  
 Db 1167 AMTSISVLPFWTIRPFTVKNIGDTSHPRLQCHFTSMWDHGVDPDTDLINRVLVRYDM 1226  
 QY 384 RKSHTTGLLVHCSAGVGTGVYICVDVYFAIEKKNYSFDIMNVYQMRKQRCGMITKEQ 443  
 Db 1227 KQSPSPPLVHCSAGVGTGVYICVDVYFAIEKKNYSFDIMNVYQMRKQRCGMITKEQ 443

QY 444 OYCFCEIVLEVLON 458  
Db 1287 QVFNQCVLIVRS 1301

## RESULT 13

S51005  
protein-tyrosine-phosphatase (EC 3.1.3.48) 2E - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 10-Apr-1996 #sequence\_revision 03-May-1996 #text\_change 22-Jun-1999  
C:Accession: S51005; S51161  
R.L.'Abbe, D.; Banville, D.; Tong, Y.; Stocco, R.; Maeson, S.; Ma, S.; Fantus, G.; Shen, P.E.S. Lett. 356, 351-356, 1994  
A:Title: Identification of a novel protein tyrosine phosphatase with sequence homology to A:Reference number: S51005; MIMD:95104449; PMID:7803871  
A:Accession: S51005  
A:Molecule type: mRNA  
A:Residues: 1-1175 <LAA>  
A:Cross-references: EMBL:U17971; NID:g662113; PIDN:AAA62153.1; PID:g602255  
A:Genetics: PTP2E  
A:Accession: S51161  
A:Molecule type: mRNA  
A:Residues: 840-1175 <IAB>  
A:Cross-references: EMBL:U18293; NID:g603228; PIDN:AAA62154.1; PID:g603229  
A:Genetics: PTP2B1  
A:Genetics: <PTP2B>  
A:Genetics: <PTP2B>  
A:Genetics: <PTP2B>  
A:Note: clone PTP2B1  
A:Note: clone PTP2B1  
C:Supernatant: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-h C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase F.2.3.304/Domain: protein 4.1 membrane-binding domain homology <B41>  
F.2.3.304/Domain: protein 4.1 membrane-binding domain homology <B41>  
F.1109/Active site: Cys (phosphotyrosine intermediate) #status predicted  
F.1115/Binding site: substrate phosphate (Arg) #status predicted

Query Match 19.9%; Score 484.5; DB 2; Length 1175;  
Best Local Similarity 28.2%; Pred. No. 1.3e-26;  
Matches 146; Conservative 69; Mismatches 141; Indels 161; Gaps 17;

QY 81 IFGNMSENKRP-----SHHLSFSDKELVYVPEPLESDPTDPTWMDSDSLNRMMSM 134  
Db 677 VPSDKVKGSTEGQSGYSHKSLSDATLHILH-----SSEDS--DSDSDSEHVAVS 729  
QY 135 DSETAG-----PSKTVSPV-----LSSGSLSKD-----TET----- 161  
Db 730 PRLTAFAFSGOQLNYPGASVTPYGPPLHIFPKSHVTEPRKADISPVLVMEHQPRR 789  
QY 162 -----SVSEKELQIAQIRPLINSSASAMRDL-----NTLQ----- 195  
Db 790 HGLLPMSSESDLTGSKYR-----ARRSLKKRPVSLSGKMTVEGLPLPG 839  
QY 196 -KKEELDIIR-----EFLLEQMTLPDDFNSGNL----- 224  
Db 840 MKKTRADAKKIGPLKLAALNGLSLRPLPDEKGVSTRANDRCVLEORLEQIVFT 899  
QY 225 -----QNFDKRYRDLIYDSTRVPLGKKD-----YINASTIRI 259  
Db 900 EYERILKKELVDGCESTARLPENNERKRFQVLPYDARVELVPTKENNTYINASHIKV 959  
QY 260 VNHBEFYIATQGPLPETHEDFQOMVLNNKCNVIAMITREIEGCVIKCVSYWPTSLKSP 319  
Db 960 SVSISLMDYIATQGPLNCTODFQOMWEGQVAILIIVNTAELEGREKSPRYMP-----R 1014  
QY 320 LEFHFVSFLETFHTVTF-----TVRVFQIVKSGTSGQCVKELQFTKMPDHGTPAS 372  
Db 1015 LGSNNTVTVYGRFKITTRFRDSCYATTLQKMGHLLTGGERVTWMLQYTDWBEHGPCPD 1074  
QY 373 ADFPKTVRYV-----RKSHING-----PLTVHCSAGVPTGTFICVDVFAIKKYS 421  
Db 1075 LKGLSLTLEELQSRKRTNSTSEPRSPPLVHCSAGVGTGVIILSITVACLENREV 1134  
QY 422 FDIWIVTQMKRQCGMIQTKQYQCFCEIVLEVLON 458

Db 1135 LDIPRVELLRQQRKMLVQTLISQYTFVRYVLQPLKS 1171

## RESULT 14

hypothetical protein K04D7.4 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T23308  
R.Wild, A.  
submitted to the EMBL Data Library, February 1996  
A:Reference number: Z19725  
A:Accession: T23308  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1156 <MTL>  
A:Cross-references: EMBL:Z69664; PIDN:CAA93513.1; GSPDB:GN00022; CESP:K04D7.4  
A:Experimental source: clone K04D7  
A:Genetics:  
A:Gene: CESP:K04D7.4  
A:Map position: 4  
A:Introns: 89/3; 153/1; 201/2; 390/3; 422/1; 482/2; 508/3; 552/1; 631/1; 721/3; 766/3;  
Query Match 19.8%; Score 484; DB 2; Length 1156;  
Best Local Similarity 27.9%; Pred. No. 1.4e-26;  
Matches 144; Conservative 84; Mismatches 202; Indels 86; Gaps 17;

QY 3 SPFRVKGKTGRNDE-----EKGNSG-----NIMLNSL-----PSSSQMTPTKV 44  
Db 432 SASITKSGAQSDVSAQTVGEGTVTFQDLNFDCKNGVKLWNVBPVSXKSPFTV 491  
QY 45 ONKMLKYEHHDLWVFLIKTIWVAVFLMKGLIFGKKNSEN-----VKPSHL 97  
Db 492 KATVQTTSLQPTTMSLDIILSLDYETL---RIVLERSTIDNSTILIGKYSDSHQF 548  
QY 98 SPSDK--YELVYVPEPLESDPTDPTWMDSDSLNRMNSMDSETAGPSEKTVSP----- 147  
Db 549 ILMDKSGYSGFSPGKCAKL-----SSAGNRYISVLIVIRAIL 590

QY 148 -----VLSGSLSLKDTTSVSEK--LTQLAQIRPLINSSAR-----SARDCIANTL 194  
Db 591 IFAPICFVIYHFRGSMNFHLLRKKEKCVYLEIEISLVYDAGQEDIPVLEFGYEDL 650  
QY 195 OKKEELDIIRFLEQMTLP--DFFNSG-----NTLQNRDKNRYRDLIYDSTRVPLSK-- 247  
Db 651 NRNDLSLKTQFQLLSQTSIGDVSGBSSSDNSQNRNNICATIRLNSPT 710  
QY 248 NKDIYINASYIRIVNHBEFYIATQGPLPETHEDFQOMVLNNKCNVIAMITREIEGCVIK 307  
Db 711 GNDYINANNVYDSCN--ERNAYIATQAPLESTFSDPMSMIQBERSNITIVCTINVEDGKRX 768  
QY 308 CYSYMPSLKEPLFEPHFVSFLETFHTVTFVTVRV--FQIVKSGTSGQCVKELQFTKMP 365  
Db 769 CDQYWSQDSDPTFGKTYQVTLVSESTNAFSLRILDLIKAVPRAVERVHQLHFGWP 828  
QY 366 DHCSTPADPFIKYRVYRKSHITGLPLVHCSAGVGTGTFICVDVFAIKKYSFDM 425  
Db 829 DHCVPSSVPEPLSFVHYTSDIHSTGTVVHCSAGVRSGLIYVD---SMRRLISPRRL 885  
QY 426 NI---VTQMKRQCGMIQTKQYQCFCEIVLEVLON 458  
Db 886 NVQGHLPKRRQAKLVQTLQYTFCHALRQILRH 921

## RESULT 15

I50212  
protein-tyrosine-phosphatase (EC 3.1.3.48) - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jan-2000  
C:Accession: I50212  
R/Stoker, A.W.  
Mech. Dev. 46, 201-217, 1994





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## OM protein - protein search, using sw model

Run on: June 18, 2004, 19:32:33 ; Search time 17 Seconds  
(without alignments)  
1418.146 Million cell updates/sec

Title: US-09-095-478a-6  
Sequence: 1 MSSPRKRYKRGKGRNDDEEG.....QYQPCRYVLEVLQNLALY 463

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Database : SwissProt\_42.\*  
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	639.5	26.2	2485	1	PTND_HUMAN
2	519	21.3	1187	1	PTNE_HUMAN
3	501	20.5	913	1	PTN3_HUMAN
4	497	20.4	1189	1	PTNE_MOUSE
5	496.5	20.4	1948	1	PTNS_HUMAN
6	487	20.0	926	1	PTN4_HUMAN
7	487	20.0	1337	1	PTP1_HUMAN
8	484.5	19.9	1175	1	PTNL_RAT
9	483.5	19.8	1439	1	PTPK_HUMAN
10	481.5	19.7	1463	1	PTPT_HUMAN
11	481.5	19.7	1912	1	PTPD_HUMAN
12	481	19.7	1176	1	PTNL_MOUSE
13	477.5	19.6	1457	1	PTPK_MOUSE
14	475	19.5	1238	1	PTPX_MOUSE
15	473.5	19.4	1454	1	PTPT_MOUSE
16	472	19.4	1377	1	PTPM_MOUSE
17	471.5	19.3	1174	1	PTNL_HUMAN
18	470	19.3	2316	1	PTPZ_RAT
19	468	19.2	1452	1	PTPM_HUMAN
20	467.5	19.2	1897	1	PTPZ_HUMAN
21	467	19.1	2314	1	PTPZ_HUMAN
22	466.5	19.1	415	1	PTN2_HUMAN
23	466	19.1	377	1	PTP2_DICDI
24	466	19.1	1452	1	PTPM_MOUSE
25	462	18.9	1216	1	PTPO_HUMAN
26	461	18.9	382	1	PTN2_MOUSE
27	459	18.8	363	1	PTN2_RAT
28	457	18.7	1255	1	CD45_RAT
29	456	18.7	780	1	PTNC_HUMAN
30	452.5	18.6	360	1	PTN7_HUMAN
31	451.5	18.5	434	1	PTN1_CHICK
32	450	18.5	1152	1	CD45_MOUSE
33	449	18.4	2029	1	LAR_DROME

34	448	18.4	775	1	PTNC_MOUSE	P35831	mus musculus
35	447	18.3	1445	1	PTPG_HUMAN	P23470	homo sapien
36	445	18.2	1304	1	CD45_HUMAN	P08575	homo sapien
37	444	18.2	2200	1	LAR_CAEEL	Q9bmm8	caenorhabdi
38	443.5	18.2	1026	1	PTPI_CAEEL	P18031	homo sapien
39	443	18.2	435	1	PTN7_HUMAN	P49445	rattus norv
40	442.5	18.1	359	1	PTN7_RAT	Q63475	rattus norv
41	440	18.0	1004	1	PTPX_RAT	P20417	rattus norv
42	439	18.0	432	1	PTN3_HUMAN	P43378	homo sapien
43	438	18.0	593	1	PTN3_MOUSE	P35821	mus musculus
44	437	17.9	432	1	PTN1_MOUSE	P41499	rattus norv
45	433.5	17.8	593	1	PTN3_RAT		

## ALIGNMENTS

RESULT 1  
ID PTND\_HUMAN STANDARD: PRT: 2485 AA.  
AC Q12923; Q15159; Q15263; Q15264; Q15265; Q15674; Q16826; Q81WH7;  
AC Q9NYN9;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Protein tyrosine phosphatase, non-receptor type 13 (EC 3.1.3.48)  
DE (Protein-tyrosine phosphatase, 1B) (PTP-El) (PTPRL) (PTP-BAS)  
DE (Protein-tyrosine phosphatase PTPRL) (Fas-associated protein-tyrosine phosphatase 1) (FAP-1).  
GN PTPN13 OR PTP13 OR PTP1 OR PNP1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 4).  
RC TISSUE=Breast carcinoma;  
RX MEDLINE=94350988; PubMed=8071359;  
RA Banville D., Ahmad S., Stocco R., Shen S.-H.;  
RT "A novel protein-tyrosine phosphatase with homology to both the cytoskeletal proteins of the band 4.1 family and junction-associated granulate kinases.";  
RL J. Biol. Chem. 269:22320-22327(1994).  
RN [2]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RC TISSUE=Leukemia;  
RX MEDLINE=94116679; PubMed=8287977;  
RA Mekawa K., Imagawa N., Nagamatsu M., Harada S.;  
RT "Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane-binding domain and GIGF repeats.";  
RL FEBS Lett. 337:200-206(1994).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fibroblast;  
RX MEDLINE=95014139; PubMed=7929060;  
RA Serra J., Claesson-Welsh L., Heldin C.-H., Guez L.J.;  
RT "Cloning and characterization of PTPBL, a protein tyrosine phosphatase with similarities to cytoskeletal-associated proteins.";  
RL J. Biol. Chem. 269:24082-24089(1994).  
RN [4]  
RP SEQUENCE OF 1216-2490 FROM N.A.  
RC TISSUE=Pancereas;  
RL Wang H.Y.;  
RN Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE OF 1279-1883 FROM N.A. (ISOFORM 4).  
RC TISSUE=Brain;  
RX MEDLINE=95232528; PubMed=7536343;  
RA Sato T., Irie S., Kitada S., Reed J.C.;  
RT "FAP-1: a protein tyrosine phosphatase that associates with Fas.";  
RL Science 268:411-415(1995).  
RN [6]  
RP SEQUENCE OF 1323-1821 FROM N.A.

RA Irie S., Hachiya T., Sato T.A.;  
 RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.  
 RN [7]  
 RP SEQUENCE OF 1323-1922 FROM N.A.  
 RC TISSUE=Eye;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Sherman C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh S.,  
 RA Dichtenko L., Marnett L., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stabileon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Iqbal N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Mizny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfield G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Rodriguez Y.S.N., Krzywinski M.I., Skalska U., Smalheuer D.E.,  
 RA Scherch A., Schin J.B., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [8]  
 RP INTERACTION WITH TRIP6.  
 RX MEDLINE=99329089; PubMed=10400701;  
 RA Murthy K.K., Clark K., Fortin Y., Shen S.-H., Banville D.;  
 RT "ZRP-1, a zyxin-related protein, interacts with the second PDZ domain  
 RT of the cytosolic protein tyrosine phosphatase hPTP.";  
 RL J. Biol. Chem. 274:20679-20687(1999).  
 RN [9]  
 RP INTERACTION WITH NGR.  
 RX MEDLINE=20012928; PubMed=10544233;  
 RA Irie S., Hachiya T., Rabizadeh S., Maruyama W., Mukai J., Li Y.,  
 RA Reed J.C., Bredeben D.E., Sato T.A.;  
 RT "Functional interaction of Fas-associated phosphatase-1 (FAP-1) with  
 RT p75(NTR) and their effect on NF-kappaB activation.";  
 RL FEBS Lett. 460:191-198(1999).  
 RN [10]  
 RP STRUCTURE BY NMR OF 1361-1456 UNCOMPLEXED AND IN COMPLEX WITH THE  
 RP C-TERMINUS OF TNFRSF6.  
 RX MEDLINE=20170882; PubMed=10704206;  
 RA Kozlov G., Gehring K., Ekkel I.;  
 RT "Solution structure of the PDZ domain from human phosphatase hPTP  
 RT and its interactions with C-terminal peptides from the Fas  
 RT receptor.";  
 RL Biochemistry 39:2572-2580(2000).  
 RN [11]  
 RP STRUCTURE BY NMR OF 1361-1456 IN COMPLEX WITH THE C-TERMINUS OF THE  
 RP GUANINE NUCLEOTIDE EXCHANGE FACTOR RA-GEF-2.  
 RX MEDLINE=22090786; PubMed=12095257;  
 RA Kozlov G., Banville D., Gehring K., Ekkel I.;  
 RT "Solution structure of the PDZ domain from cytosolic human  
 RT phosphatase hPTP in complex with a peptide reveals contribution of  
 RT the beta2-beta3 loop to PDZ domain-ligand interactions.";  
 RL J. Mol. Biol. 320:813-820(2002).  
 RN [12]  
 RP VARIANTS PRO-1419 AND MET-1522.  
 RX MEDLINE=22323362; PubMed=12436199;  
 RA Yoshida S., Harada H., Nagai H., Fukino K., Teramoto A., End M.;  
 RT "Head-to-head juxtaposition of Fas-associated phosphatase-1 (FAP-1)  
 RT and c-Jun NH2-terminal kinase 3 (JNK3) genes: genomic structure and  
 RT seven polymorphisms of the FAP-1 gene.";  
 RL J. Hum. Genet. 47:614-619(2002).  
 CC -1- FUNCTION: Regulates negatively Fas-induced apoptosis and NGR-  
 CC mediated proapoptotic signaling.  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -1- SUBUNIT: Interacts with TRIP6 and TNFRSF6 (Fas receptor) through  
 CC its second PDZ domain. Interacts with the C-terminal SVP motif of

CC NGR through its third PDZ domain.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=1;  
 CC IsoId=Q12923-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q12923-2; Sequence=VSP\_000496;  
 CC Name=3;  
 CC IsoId=Q12923-3; Sequence=VSP\_000497;  
 CC Name=4;  
 CC IsoId=Q12923-4; Sequence=VSP\_007921;  
 CC Note=May be due to a competing donor splice site;  
 CC -1- TISSUE SPECIFICITY: Present in most tissues with the exception of  
 CC the liver and skeletal muscle. Most abundant in lung, kidney and  
 CC fetal brain.  
 CC -1- SIMILARITY: Contains 1 PRRM domain.  
 CC -1- SIMILARITY: Contains 5 PDZ/DHR domains.  
 CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.  
 CC Non-receptor class subfamily.  
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 CC -----  
 CC EMBL: U12128; AAB60339.1; -  
 CC EMBL: D21209; BAA04750.1; -  
 CC EMBL: D21210; BAA04751.1; -  
 CC EMBL: D21211; BAA04752.1; -  
 CC EMBL: X80289; CA556563.1; -  
 CC EMBL: X79676; CA556124.1; -  
 CC EMBL: L34583; AAC41755.1; -  
 CC EMBL: AF233323; AAF63474.1; -  
 CC EMBL: BC039610; AAH39610.1; ALT\_TERM.  
 CC EMBL: A54971; A54971.  
 CC PIR: I67629; I67629.  
 CC PIR: I67630; I67630.  
 CC PDB: 3PDZ; 17-MAR-00.  
 CC PDB: 1D5G; 24-JUL-02.  
 CC Gene: HGNC:9646; PTPN13.  
 CC MM: 600267; -  
 CC GO: GO:0004725; P:protein tyrosine phosphatase activity; TAS.  
 CC GO: GO:0006470; P:protein amino acid dephosphorylation; TAS.  
 CC InterPro: IPR000299; Band\_4.1.  
 CC InterPro: IPR001478; PDZ.  
 CC InterPro: IPR000367; Tyr\_PP.  
 CC InterPro: IPR000242; Tyr\_PP.  
 CC Pfam: PF00373; Band\_41; 1.  
 CC Pfam: PF00595; PDZ; 5.  
 CC Pfam: PF0102; Y\_phosphatase; 1.  
 CC PRINTS: PR00935; BAND41.  
 CC PRINTS: PR00700; PRYHPPTASE.  
 CC SMART: SM00295; B41; 1.  
 CC SMART: SM00228; PDZ; 5.  
 CC SMART: SM00194; PTPC; 1.  
 CC PROSITE: PS00660; PRRM\_1; FALSE\_NEG.  
 CC PROSITE: PS00661; PRRM\_2; FALSE\_NEG.  
 CC PROSITE: PS00577; PRRM\_3; 1.  
 CC PROSITE: PS0106; PDZ; 5.  
 CC PROSITE: PS00363; TYR\_PHOSPHATASE\_1; FALSE\_NEG.  
 CC PROSITE: PS00566; TYR\_PHOSPHATASE\_2; 1.  
 CC PROSITE: PS00565; TYR\_PHOSPHATASE\_PTP; 1.  
 CC Structural protein; Cytoskeleton; Hydrolyase; Repeat; 3D-structure;  
 CC Alternative splicing; Coiled coil; Polymorphism.  
 CC DOMAIN 56 59 POLY-LEU.  
 CC DOMAIN 572 872 PRRM.  
 CC DOMAIN 2237 2485 PROTEIN-TYROSINE PHOSPHATASE.  
 CC DOMAIN 379 399 COILED COIL (POTENTIAL).  
 CC DOMAIN 469 504 COILED COIL (POTENTIAL).

Query Match 26.2%; Score 619.5; DB 1; Length 2485;  
 Best Local Similarity 37.8%; Pred. No. 5.8e-37;  
 Matches 137; Conservative 62; Mismatches 128; Indels 35; Gaps 6;

QY 108 PEPLESDTEVWVSDSLRNKNSMDETAAGPSKTVSPVLSGSSRLXCTETNSVSEKE 167  
 DB 2139 POKKTDDELITWG-NDLPIERTTHESD-----KD-HSLTND 2177  
 QY 168 LTQALQIRPLIFNSASASMDCLNTLO-----KKELDIIEEPLLEQMTLPDDFNS 220  
 DB 2178 LAVIPVAVPLPSGKTGALNSKVRVLRGLLDGQIPSEKLENLDELKPLDCLL----- 2221  
 QY 221 GNTLONRKNRYDLPDSTRVPLGKKNKDYNSYRIVNHSEEFYIAQGLPTIE 260  
 DB 2232 GQTKENRKNRYKILPDAIRVPLGDBGYINSPFLIPVKEEFYIAQGLPTTVG 2291  
 QY 281 DFMQVLENNKCVIAMIITREIBGVIKCYSPYSL-KEPLPEHFSVLETFHYOYFT 339  
 DB 2292 DFMQVLENNKCVIAMIITREIBGVIKCYSPYSL-KEPLPEHFSVLETFHYOYFT 2351  
 QY 340 VRVQIVKSGKSGQCVNHLQPTKPHGTASADFLIKVRYKXSHITGPLLVHGSAG 399  
 DB 2352 VRAMTLEIDITREVRHISHNLFTAMPDHPDPSQDDLLFTISYKRAHRSQPIITHCSAG 2411  
 QY 400 VGRGVFICVDVVSALIKNSYFDIMNIVTOMRQKRCGMITKEQYQFCYEVLEVONL 459  
 DB 2412 IGRSGTLCIDIVVAGLISQDLPDISLVRCMRLOHGMVQTEBDQIFCYVILVLTSL 2471  
 QY 460 LA 461  
 DB 2472 QA 2473

## RESULT 2

PTNE\_HUMAN STANDARD; PRT; 1187 AA.

AC Q15678;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein tyrosine phosphatase, non-receptor type 14 (EC 3.1.3.48)  
 DE (Protein-tyrosine phosphatase pty).  
 OS PTN14 OR P2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Breast carcinoma;  
 RX MEDLINE=9525172; PubMed=7733990;  
 RA Smith A.L., Mitchell P.J., Shipley J., Gusterson B.A., Rogers M.V.,  
 RA Cremonesi M.R.;  
 RT "Pty: a novel human cDNA encoding protein tyrosine phosphatase- and  
 RT ezrin-like domains";  
 RT Biochem. Biophys. Res. Commun. 209:959-965(1995).  
 RL -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -1- TISSUE SPECIFICITY: Expressed in a variety of human tissues  
 CC including kidney, skeletal muscle, lung and placenta.  
 CC -1- SIMILARITY: Contains 1 PFM domain.  
 CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.  
 CC Non-receptor class subfamily.

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DR EMBL; X82676; CA57993.1; --  
 DR PIR; J04155; J04155.  
 DR HSSP; P29350; 1GM2.  
 DR Genew; HGNC:9647; PTPN14.  
 DR MIM; 603155; --  
 DR CO; GO:0004725; P:Protein tyrosine phosphatase activity; TAS.  
 DR CO; GO:0006470; P:Protein amino acid dephosphorylation; TAS.  
 DR InterPro; IPR000299; Band 4.1.  
 DR InterPro; IPR000387; Tyr\_phosphatase.  
 DR InterPro; IPR000242; Tyr\_PP.  
 DR Pfam; PF00373; Band 4.1; 1.  
 DR Pfam; PF00102; Y\_phosphatase; 1.  
 DR PRINTS; PR00935; BAND4.1.  
 DR PRINTS; PR00700; PRTYPTPHASE.  
 DR SMART; SM00295; B4.1; 1.  
 DR SMART; SM00194; PTPC; 1.  
 DR PROSITE; PS00660; FERM\_1; 1.  
 DR PROSITE; PS00661; FERM\_2; 1.  
 DR PROSITE; PS00657; FERM\_3; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_FTP; 1.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
 DR KEGG; Structural protein; Cytoskeleton; Hydrolyase.  
 PT DOMAIN 21 306 FERM.  
 PT ACT\_SITE 933 1187 PROTEIN-TYROSINE PHOSPHATASE.  
 PT ACT\_SITE 1121 1121 PHOSPHOCYSTEINE INTERMEDIATE  
 (BY SIMILARITY).  
 FT DOMAIN 566 573 POLY-PRO.  
 FT DOMAIN 709 716 POLY-GLU.  
 SQ SEQUENCE 1187 AA; 135239 MW; 015760B75E3574E3 CRC64;

Query Match 21.3%; Score 519; DB 1; Length 1187;  
 Best Local Similarity 32.0%; Pred. No. 7.1e-29;  
 Matches 143; Conservative 65; Mismatches 129; Indels 110; Gaps 14;

QY 107 YPEPLESDTEVWVSDSLRNKNSMDETA-----GPEKTVS-----PVLSSGS 153  
 DB 752 YPGPRKS-----VSNGLRQDQALPAMARAVLRHGPAAKALSMSTRTPDPANVGAS 803  
 QY 154 -RLSKQETYSYSEK-----ELTOL-----AQR 175  
 DB 804 LGSSTIEPDLTVKKEVYKGPYKERVSMFLEDSIIRRMIRLEKQXAGLENOQR 863  
 QY 176 PLIFNS-----SASARDCLNTLOK-BELDIIRSELEQMTLPD 216  
 DB 864 PLTALINGLSVARVSGREENVDATRVPMDFRTKCKLEKGVFTYEQIPKKKAG 923  
 QY 217 DPNSGNTLONRKNRYDLPDSTRVPL-----GKKQYINASYRIVNHSEEFYIAQ 272  
 DB 924 IFTALPENAERSRIRREVPEENKVELIPKENNTGYINASHIKVAVGGAEMHYIATQ 983  
 QY 273 GPLPETIDFMQVLENNKCVIAMIITREIEGVIKCYSPYSLKPELFEHFSVLETF 332  
 DB 984 GPLPETIDFMQVLENNKCVIAMIITREIEGVIKCYSPYSLKPELFEHFSVLETF 332  
 QY 333 HTQYVTVAVPQVAKSF-----GKSQCYKHLQPTKPHGTASADFLIKY----- 379  
 DB 1039 KATTFE-RTDSVCYATFGLKVKHLLSGQERTVMHLQYTDWBDHGGPEVDQGLSTLEBI 1096  
 QY 380 -VRVYRKSHNG-----PLLVHCSAGAGRGVFCVDVVSALIKNSYFDIMNIVTOM 431  
 DB 1097 GSVRRHTNMLMGSTGNRHPRIYVHCSAGAGRGVILLSLMVLCLEHNEKVEVPMMLRL 1156  
 QY 432 RKQRCGMITKEQYQFCYEVLEVON 458  
 DB 1157 RQRMRMTQTIAQYKRVYVGLIQFLON 1183

## RESULT 3

PTN3\_HUMAN STANDARD; PRT; 913 AA.

ID PTN3\_HUMAN  
 AC P26045;  
 DT 01-MAY-1992 (Rel. 22, Created)

01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein tyrosine phosphatase, non-receptor type 3 (EC 3.1.3.48)  
 DB (Protein-tyrosine phosphatase H1) (PTP-H1).  
 GN PTPN3 OR PTPH1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91296738; PubMed=1648725;  
 RA Yang Q., Tonks N.K.;  
 RT "Isolation of a cDNA clone encoding a human protein-tyrosine  
 phosphatase with homology to the cytoskeletal-associated proteins  
 band 4.1, ezrin, and talin.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:5949-5953(1991).  
 RN [2]  
 RP SEQUENCE OF 194-896 FROM N.A.  
 RX TISSUE=Colon;  
 CC MEDLINE=92327504; PubMed=1626183;  
 RA Aizawa Y., Hinda Y., Itoh F., Takekawa M., Tsujisaki M., Adachi M.,  
 RA Imai K., Yachi A.;  
 RT "cDNA cloning of new protein tyrosine phosphatases in the human  
 colon.";  
 RL Tumour Biol. 13:180-186(1992).  
 RN [3]  
 RP SEQUENCE OF 899-913 FROM N.A.  
 RX MEDLINE=95179278; PubMed=7874267;  
 RA Ikuta S., Itoh F., Hinda Y., Toyota M., Makiguchi Y., Imai K.,  
 RA Yachi A.;  
 RT "Expression of cytoskeletal-associated protein tyrosine phosphatase  
 PTPH1 mRNA in human hepatocellular carcinoma.";  
 RL J. Gastroenterol. 29:727-732(1994).  
 CC -1- FUNCTION: May act at junctions between the membrane and the  
 cytoskeleton.  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 tyrosine + phosphate.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.  
 CC -1- SIMILARITY: Contains 1 FERM domain.  
 CC -1- SIMILARITY: Contains 1 PDZ/DRH domain.  
 CC  
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DR PROSITE: PS00660; FERM\_1; 1.  
 DR PROSITE: PS00661; FERM\_2; 1.  
 DR PROSITE: PS00662; FERM\_3; 1.  
 DR PROSITE: PS00663; FERM\_4; 1.  
 DR PROSITE: PS00664; FERM\_5; 1.  
 DR PROSITE: PS00665; FERM\_6; 1.  
 DR PROSITE: PS00666; FERM\_7; 1.  
 DR PROSITE: PS00667; FERM\_8; 1.  
 DR PROSITE: PS00668; FERM\_9; 1.  
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 DR PROSITE: PS01078; FERM\_419; 1.  
 DR PROSITE: PS01079; FERM\_420; 1.  
 DR PROSITE: PS01080; FERM\_421; 1.  
 DR PROSITE: PS01081; FERM\_422; 1.  
 DR PROSITE: PS01082; FERM\_423; 1.  
 DR PROSITE: PS01083; FERM\_424; 1.  
 DR PROSITE: PS01084; FERM\_425; 1.  
 DR PROSITE: PS01085; FERM\_426; 1.  
 DR PROSITE: PS01086; FERM\_427; 1.  
 DR PROSITE: PS01087; FERM\_428; 1.  
 DR PROSITE: PS01088; FERM\_429; 1.  
 DR PROSITE: PS01089; FERM\_430; 1.  
 DR PROSITE: PS01090; FERM\_431; 1.  
 DR PROSITE: PS01091; FERM\_432; 1.  
 DR PROSITE: PS01092; FERM\_433; 1.  
 DR PROSITE: PS01093; FERM\_434; 1.  
 DR PROSITE: PS01094; FERM\_435; 1.  
 DR PROSITE: PS01095; FERM\_436; 1.  
 DR PROSITE: PS01096; FERM\_437; 1.  
 DR PROSITE: PS01097; FERM\_438; 1.  
 DR PROSITE: PS01098; FERM\_439; 1.  
 DR PROSITE: PS01099; FERM\_440; 1.  
 DR PROSITE: PS01100; FERM\_441; 1.  
 DR PROSITE: PS01101; FERM\_442; 1.  
 DR PROSITE: PS01102; FERM\_443; 1.  
 DR PROSITE: PS01103; FERM\_444; 1.  
 DR PROSITE: PS01104; FERM\_445; 1.  
 DR PROSITE: PS01105; FERM\_446; 1.  
 DR PROSITE: PS01106; FERM\_447; 1.  
 DR PROSITE: PS01107; FERM\_448; 1.  
 DR PROSITE: PS01108; FERM\_449; 1.  
 DR PROSITE: PS01109; FERM\_450; 1.  
 DR PROSITE: PS01110; FERM\_451; 1.  
 DR PROSITE: PS01111; FERM

## Non-receptor class subfamily.

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DR EMBL: D11842; BAA06628.1; -  
DR PIR: JC2366; JC2366.  
DR HSSP: O06124; 2SHP.  
DR MGD: MG1:102467; Ptpn14.  
DR InterPro: IPR000299; Band 4.1.  
DR InterPro: IPR000387; Tyr\_phosphatase.  
DR InterPro: IPR000242; Tyr\_PP.  
DR Pfam: PF00373; Band 4.1; 1.  
DR Pfam: PF00102; Y\_phosphatase; 1.  
DR PRINTS: PR00935; BAND4.1.  
DR PRINTS: PR00700; PRTYHPHTASE.  
DR SMART: SM00295; B4.1; 1.  
DR SMART: SM00194; FTEP; 1.  
DR PROSITE: PS00660; FERM 1; 1.  
DR PROSITE: PS00661; FERM 2; 1.  
DR PROSITE: PS00057; FERM 3; 1.  
DR PROSITE: PS00383; TYR\_PHOSPHATASE\_PTP; 1.  
DR PROSITE: PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
DR PROSITE: PS00056; TYR\_PHOSPHATASE\_2; 1.  
DR Structural protein; Cytoskeleton; Hydrolyase.  
FT DOMAIN 21 306 FERM.  
FT ACT\_SITE 935 1189 PHOSPHOCYSTEINE INTERMEDIATE.  
FT 1123 1123 (BY SIMILARITY).  
FT DOMAIN 565 573 POLY-PRO.  
FT DOMAIN 635 639 POLY-GLY.  
FT DOMAIN 712 718 POLY-GLU.  
SQ SEQUENCE 1189 AA; 135030 MW; 2B85B5F9C723303 CRC64;  
Query Match 20.4%; Score 497; DB 1; Length 1189;  
Best Local Similarity 32.4%; Pred. No. 2,6e-27;  
Matches 128; Conservative 64; Mismatches 125; Indels 78; Gaps 11;

QY 133 SMDSETPKPSKTVSPVLSSGSRSLKSD-----TETSVSEKELT----- 169  
DB 800 AVNGASISGPSISBPDLSVSKRVKKEPVKRPVSEMSLEDSILIEREMMIRNLEKQMTG 859  
QY 170 QLAQIRPLIF-----NSSASASAMDCNTLOKXELDIIRPELEQ 211  
DB 860 PQAKRPLKLAALNGLSVARVSGEDGRHDITRPIDRLRALKKKLEQGV--FTEYEQ 917  
QY 212 WLPDD-----FNSGNTLQNNKKNRYDIPYDSTRVPL-----GKNQYINASYIRLVN 262  
DB 918 --IPNKKANGVFSATLPENASERSIRBVPYENRVELLPTKENMNGYINASHIKVVG 975  
QY 263 BBEFYATGCPLETEDPQWVLENNCVIAMIIEIGYKCYSPFISKEPLEF 322  
DB 976 GSEMYIATGCPLETEDPQWVLENNCVIAMIIEIGYKCYSPFISKEPLEF 322  
QY 323 EHFSEVPLETHVTOYF-----TVRFQIVKSTGSCCKHLOFTKPDHGTASADP 375  
DB 1031 KHSATYVGKFKVTTKFTDSCGVAITGLKTKHLLSGERTVNLHLYIDWPHHCSPRYVG 1090  
QY 376 FIKY-----VRYRKSHITG-----PLLVHCSAGVGRGVICVDVFSALIKNSFD 423  
DB 1091 FLSYLEIIGSVRRHTNSVLSGIRFRAPPIVHCSAGVGRGVILSELIMTYCLEHNEKVE 1150  
QY 424 INAVITQMRKQRCGMITQEQYOFCYEIVLEVLON 458  
DB 1151 VPTMLRRLRQRMFMITQINQYFVGVVLOFLO 1185

RESULT 5

PTNS HUMAN  
ID PTNS HUMAN STANDARD; PRT; 1948 AA.  
AC Q13332; Q15718; Q16341;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Receptor-type protein-tyrosine phosphatase S precursor (EC 3.1.3.48)  
DE (R-PTP-S) (Protein-tyrosine phosphatase sigma) (R-PTP-sigma).  
GN PTPS.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fetal brain;  
RX MEDLINE=96102179; PubMed=8524829;  
RA Pulido R., Serra-Pages C., Tang M., Streuli M.;  
RT "The LAR/PTP delta/PTP sigma subfamily of transmembrane protein-  
RT tyrosine-phosphatases: multiple human LAR, PTP delta, and PTP sigma  
RT isoforms are expressed in a tissue-specific manner and associate with  
RT the LAR-interacting protein LIP-1.";  
RL Proc. Natl. Acad. Sci. U.S.A. 92:11686-11690(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9625038; PubMed=8992885;  
RA Endo N., Rutledge S.J., Opas E.B., Vogel R., Rodan G.A., Schmidt A.;  
RT "Human protein tyrosine phosphatase-sigma: alternative splicing and  
RT inhibition by bisphosphonates.";  
RL J. Bone Miner. Res. 11:535-543(1996).  
RN [3]  
RP SEQUENCE OF 1-126 FROM N.A.  
RA Lemerding J.E., McCreedy P.M., Skowronski E., Viswanathan V.,  
RA Burkhardt-Schultz K., Gordon U., Dias J., Ramirez M., Stelwagen S.,  
RA Phan H., Velasco N., Do D., Regala W., Terry A., Ganes J.,  
RA Dangman L., Ertler A., Christensen M., Georgescu A., Avila J., Liu S.,  
RA Attix C., Andrese T., Frankel M., Amico-Keller G., Coeffield J.,  
RA Duarte S., Lucas R., Bruce R., Thomas P., Quan G., Krommiller B.,  
RA Arellano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A.,  
RA Olsen A.S., Carraro A.V.;  
RT "Sequence analysis of a 2.5 Mb region in 19p13.3,";  
RL "Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases."  
RN [4]  
RP SEQUENCE OF 1503-1589 FROM N.A.  
RX MEDLINE=92119637; PubMed=1370651;  
RA Aachi M., Sekiya M., Arimura Y., Takekawa M., Itoh F., Hinoda Y.,  
RA Imai K., Yachi A.;  
RT "Protein-tyrosine phosphatase expression in pre-B cell NALM-6,";  
RL Cancer Res. 52:737-740(1992).  
CC -1- FUNCTION: Interacts with LAR-interacting protein LIP-1.  
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
CC tyrosine + phosphate.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=5;  
CC Comment=Additional isoforms seem to exist;  
CC Name=PTPS;  
CC IsoId=Q13332-1; Sequence=Displayed;  
CC Name=PTPS-MEA;  
CC IsoId=Q13332-2; Sequence=VSP\_050021;  
CC Name=PTPS-MEB;  
CC IsoId=Q13332-3; Sequence=VSP\_050022, VSP\_050026, VSP\_050027;  
CC Name=PTPS-MEC;  
CC IsoId=Q13332-4; Sequence=VSP\_050024;  
CC Name=PTPS-F4-7;  
CC IsoId=Q13332-5; Sequence=VSP\_050025, VSP\_050025;  
CC -1- TISSUE SPECIFICITY: Detected in all tissues tested except for  
CC placenta and liver.  
CC -1- SIMILARITY: BELONGS TO THE RECEPTOR CLASS OF THE PROTEIN-TYROSINE  
CC PHOSPHATASE FAMILY.  
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domain.  
CC -1- SIMILARITY: Contains 8 fibronectin type III domains.  
CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.

```
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```

DR	EMBL;	U35234;	AAC50299.1; .-
DR	EMBL;	U43117;	AAC50567.1; .-
DR	EMBL;	AC005790;	AAC82832.1; .-
DR	HSSP;	S78080;	MAB21146.2; .-
DR	Genevex;	HGNC:	9681; PTPRS.
DR	GO;	GO:000587;	C:integral to plasma membrane; TAS.
DR	GO;	GO:0005001;	F:transmembrane receptor protein tyrosine pho...; TAS.
DR	InterPro;	IPIR003957;	FN III-like.
DR	InterPro;	IPIR003961;	FN III.
DR	InterPro;	IPIR003962;	FnIII_subd.
DR	InterPro;	IPIR007110;	IG-like.
DR	InterPro;	IPIR003598;	IG_c2.
DR	InterPro;	IPIR000387;	Tyr_phosphatase.
DR	Pfam;	PF000041;	fna3_8.
DR	Pfam;	PF000047;	lg_3.
DR	Pfam;	PP00102;	Y-phosphatase; 2.
DR	PRINTS;	PR00014;	ENTYPRIII.
DR	PRINTS;	PR00700;	PTYPEPHASE.
DR	SMART;	SMO0060;	FN3; 7.
DR	SMART;	SMO0408;	IGc2; 3.
DR	SMART;	SMO0194;	PTPC; 2.
DR	PROSITE;	PS50835;	IG LIKE; 3.
DR	PROSITE;	PS00383;	TYR_PHOSPHATASE 1; 2.
DR	PROSITE;	PS50056;	TYR_PHOSPHATASE 2; 2.
DR	PROSITE;	PS50055;	TYR_PHOSPHATASE_PTP; 2.
KM	Hydroxylase;	Receptor;	Glycoprotein; Signal; Transmembrane;
KW	Cell adhesion;	Immunoglobulin domain;	Alternative splicing; Repeat.
FT	CHAIN	1	29
FT	DOMAIN	30	1282
FT	TRANSMEME	1283	1303
FT	DOMAIN	1304	1948
FT	DOMAIN	33	123
FT	DOMAIN	135	233
FT	DOMAIN	245	327
FT	DOMAIN	329	423
FT	DOMAIN	426	522
FT	DOMAIN	525	615
FT	DOMAIN	618	717
FT	DOMAIN	720	831
FT	DOMAIN	834	926
FT	DOMAIN	928	1033
FT	DOMAIN	1036	1151
FT	DOMAIN	1333	1648
FT	DOMAIN	1680	1930
FT	DOMAIN	641	644
FT	DISULFID	54	107
FT	DISULFID	156	216
FT	DISULFID	266	311
FT	ACT_SITE	1869	1869
FT	ACT_SITE	1880	1880
FT	CARBOHYD	263	263
FT	CARBOHYD	308	308
FT	CARBOHYD	733	733
FT	CARBOHYD	940	940
FT	VARSPLIC	190	198
FT	VARSPLIC	236	239
FT	VARSPLOC	236	239

RECEPTOR-TYPE PROTEIN-TYROSINE PHOSPHATASE S.  
EXTRACELLULAR (POTENTIAL).  
CYTOPLASMIC (POTENTIAL).  
IG-LIKE C2-TYPE 1.  
IG-LIKE C2-TYPE 2.  
IG-LIKE C2-TYPE 3.  
FIBRONECTIN TYPE-III 1.  
FIBRONECTIN TYPE-III 1.  
FIBRONECTIN TYPE-III 3.  
FIBRONECTIN TYPE-III 4.  
FIBRONECTIN TYPE-III 5.  
FIBRONECTIN TYPE-III 6.  
FIBRONECTIN TYPE-III 7.  
FIBRONECTIN TYPE-III 8.  
FIBRONECTIN TYPE-III 9.  
PROTEIN-TYROSINE PHOSPHATASE 1.  
PROTEIN-TYROSINE PHOSPHATASE 2.  
POLY-PRO.  
POTENTIAL.  
POTENTIAL.  
POTENTIAL.  
PHOSPHOCSTEINE INTERMEDIATE (BY SIMILARITY).  
PHOSPHOCSTEINE INTERMEDIATE (BY SIMILARITY).  
INTERMEDIATE (BY SIMILARITY).  
N-LINKED (GLCNAC...) (POTENTIAL).  
N-LINKED (GLCNAC...) (POTENTIAL).  
N-LINKED (GLCNAC...) (POTENTIAL).  
N-LINKED (GLCNAC...) (POTENTIAL).  
Missing (in isoform PTPS-MEA).  
/FTId=VSB\_050002.  
Missing (in isoform PTPS-MEB).

Query	Subject	Score	DB	Length	Matches	Conservative	Mismatches	Indels	Gaps
Q1	1680 MELEPRLANSKAFKTSRFLISANLPCKFKRLVIMNESRVLQPIRGVSGSDYINAS	20.4%	DB	1948	109	47	90	21	7
Q2	207 LELFQMTLPD-----FNSGNTLONDKKRYRDIIEYDSTRVPLG-----KNDYINAS	49.6%	DB	1948	109	47	90	21	7
Q3	256 YIRIVNEEYFYIATQGLPETIEDFWQVNLNNCVIANITFISGVKCYSPIS	49.6%	DB	1948	109	47	90	21	7
Q4	1740 FID--GYRQKAVIATQGLPETIEDFWQVNLNNCVIANITFISGVKCYSPIS	49.6%	DB	1948	109	47	90	21	7
Q5	316 LKEPLREHNSVF--LEFHYTVQTVAVFOIVKSKTSQCVKLOFTKPDHGTSPASAD	49.6%	DB	1948	109	47	90	21	7
Q6	1796 AERSARVQYFVUDPMARYNPOYI--LEFHYTVQTVAVFOIVKSKTSQCVKLOFTKPDHGTSPASAD	49.6%	DB	1948	109	47	90	21	7
Q7	375 FFIKRYEYVRSKSH---ITGPELLHVCAGVGRGVFTICVDVPSAIEKNYSFDIMNITVQ	49.6%	DB	1948	109	47	90	21	7
Q8	1855 GFIDFIOGVHKTKEQFGQDGPISVHCAGVGRGVFTICVDVPSAIEKNYSFDIMNITVQ	49.6%	DB	1948	109	47	90	21	7
Q9	431 MEKORCGMIOTKBOYRCYRIVLEVL	49.6%	DB	1948	109	47	90	21	7
Q10	1915 LRTQRPAMVGTEDYQFCYDALETL	49.6%	DB	1948	109	47	90	21	7
Q11	1915 LRTQRPAMVGTEDYQFCYDALETL	49.6%	DB	1948	109	47	90	21	7
Q12	1915 LRTQRPAMVGTEDYQFCYDALETL	49.6%	DB	1948	109	47	90	21	7
Q13	1915 LRTQRPAMVGTEDYQFCYDALETL	49.6%	DB	1948	109	47	90	21	7
Q14	1915 LRTQRPAMVGTEDYQFCYDALETL	49.6%	DB	1948	109	47	90	21	7
Q15	1915 LRTQRPAMVGTEDYQFCYDALETL	49.6%	DB	1948	109	47	90	21	7
Q16	1915 LRTQRPAMVGTEDYQFCYDALETL	49.6%	DB	1948	109	47	90	21	7
Q17	1915 LRTQRPAMVGTEDYQFCYDALETL	49.6%	DB	1948	109	47	90	21	7
Q18	1915 LRTQRPAMVGTEDYQFCYDALETL	49.6%	DB	1948	109	47	90	21	7
Q19	1915 LRTQRPAMVGTEDYQFCYDALETL	49.6%	DB	1948	109	47	90	21	7
Q20	1915 LRTQRPAMVGTEDYQFCYDALETL	49.6%	DB	1948	109	47	90	21	7
Q21	1915 LRTQRPAMVGTEDYQFCYDALETL	49.6%	DB	1948	109	47	90	21	7
Q22	1915 LRTQRPAMVGTEDYQFCYDALETL	49.6%	DB	1948	109	47	90	21	7
Q23	1915 LRTQRPAMVGTEDYQFCYDALETL	49.6%	DB	1948	109	47	90	21	7
Q24	1915 LRTQRPAMVGTEDYQFCYDALETL	49.6%	DB	1948	109	47	90	21	7
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Q26	1915 LRTQRPAMVGTEDYQFCYDALETL	49.6%	DB	1948	109	47	90	21	7
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Q32	1915 LRTQRPAMVGTEDYQFCYDALETL	49.6%	DB	1948	109	47	90	21	7
Q33	1915 LRTQRPAMVGTEDYQFCYDALETL	49.6%	DB	1948	109	47	90	21	7
Q34	1915 LRTQRPAMVGTEDYQFCYDALETL	49.6%	DB	1948	109	47	90	21	7
Q35	1915 LRTQRPAMVGTEDYQFCYDALETL	49.6%	DB	1948	109	47	90	21	7
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Q38	1915 LRTQRPAMVGTEDYQFCYDALETL	49.6%	DB	1948	109	47	90	21	7
Q39	1915 LRTQRPAMVGTEDYQFCYDALETL	49.6%	DB	1948	109	47	90	21	7
Q40	1915 LRTQRPAMVGTEDYQFCYDALETL	49.6%	DB	1948	109	47	90	21	7

RC TISSUE=Colon; PubMed=12477932;  
 RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zolbers K.H., Schaefer B., Buetow K.H., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stepieton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McGowan P.J., Mckernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences".  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RI -1- FUNCTION: May act at junctions between the membrane and the  
 CC cytoskeleton.  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -1- SIMILARITY: Contains 1 FERM domain.  
 CC -1- SIMILARITY: Contains 1 PDZ/DHR domain.  
 CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.  
 CC Non-receptor class subfamily.  
 CC -----  
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 CC -----  
 DR EMBL: M68941; AAA6530.1; -;  
 DR EMBL: BC010674; AAH0674.1; -;  
 DR PIR: A41105; A41105.  
 DR HSSP: P29350; IGMZ.  
 DR Genem: HENC:9656; PTM4.  
 DR KIM: 176878; -;  
 DR GO: GO:0005737; C:cytoplasm; TAS.  
 DR GO: GO:0004726; F:non-membrane spanning protein tyrosine phos. .; TAS.  
 DR GO: GO:0006470; P:protein amino acid dephosphorylation; TAS.  
 DR InterPro: IPR000293; Band\_4.1.  
 DR InterPro: IPR001478; PDZ.  
 DR InterPro: IPR000387; Tyr\_phosphatase.  
 DR InterPro: IPR000242; Tyr\_PP.  
 DR Pfam: PF00373; Band\_41; 1.  
 DR Pfam: PF00595; PDZ; 1.  
 DR Pfam: PF00102; Y\_phosphatase; 1.  
 DR PRINTS: PRO0935; BAND41.  
 DR PRINTS: PRO0700; PRTYPPHPTASE.  
 DR SMART: SM00295; B41; 1.  
 DR SMART: SM00228; PDZ; 1.  
 DR SMART: SM00194; PTPC; 1.  
 DR PROSITE: PS00660; FERM\_1; 1.  
 DR PROSITE: PS00661; FERM\_2; 1.  
 DR PROSITE: PS00657; FERM\_3; 1.  
 DR PROSITE: PS00106; PDZ; 1.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE: PS00056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE: PS00055; TYR\_PHOSPHATASE\_PP; 1.  
 KM Structural protein; Cytoskeleton; Hydrolyase.  
 FT DOMAIN 29 312 FERM.  
 FT 517 589 PDZ.  
 FT DOMAIN 677 926 PROTEIN-TYROSINE PHOSPHATASE.  
 FT ACT\_SITE 852 852 PHOSPHOCYSTEINE INTERMEDIATE  
 (BY SIMILARITY).

SO SEQUENCE 926 AA; 105911 MW; 4DAC6A87A675CFB0 CRC64;  
 Query Match 20.0%; Score 487; DB 1; Length 926;  
 Best Local Similarity 28.9%; Pred. No. 9, 3e-27;  
 Matches 137; Conservative 74; Mismatches 173; Indels 90; Gaps 13;  
 QY 24 NNLRLNSLPSSGQKPTPVQKNNL-----MKKEE-----LDILMVLKLTW 69  
 DB 490 HINETDIPSPSPKPTPPNGGIPNDNLVLRKFDENGRGPNVKGIDQMPVIVRVP 549  
 QY 70 YNVEFKLKKGLIFGNK---NSSENVKPSHHSFSDCYELVPEPLSDTDE-----T 118  
 DB 550 GTPADLCVRLNGDQVVLINGRDIAEHTR---DQVLFIRKASCRHSGLKELVRPA 605  
 QY 119 VMDSPRLSRNRNSMDSTAGSKTVSPVLSGSSRLSKDTERVSEKELTQLAQIRPL 178  
 DB 606 VYDVVEEKEN-----EPDFQYIPKAPLD 630  
 QY 179 FNSASARADCLNTLQKKEE---DIREFLELBQWLPDDFNSGNTYQNRDNRYRDI 235  
 DB 631 SVYQDHSIRBSN--IQALFGLITGVTVQFDQYKRGGMSCAKLQNIKNRYRDI 688  
 QY 236 LPYDSTRVPLGKXKDYINASYR-----YVNEEYFYIATQGPLPETTEDFWQVIE 288  
 DB 689 SPYDATRVILKEDYINANYINWEIPSSSIINQ-----YIACQGPLPRTCTDFWQVIE 743  
 QY 289 NNGNVYAKITREBEGVICYGYPISTLKEPBEHFVSFLEFHYTVQVYAVPQ---I 345  
 DB 744 QSSMWVLTITVERKRVKQHWMP---EPYSSSYGYQVTCSEBGNVYIPKATL 799  
 QY 346 VKKSTKSGCVKRLQFTKMPDHGTSPASADPFIKYRYVYKSHI--TGPLLHSCAGVGT 403  
 DB 800 FQEKHSRPSPLQIQYIAMPDGVPSDDFLDFVCHVNRKAGKEPVPVHCSAGIGRT 859  
 QY 404 GYFICDVVPSALIKKYSFDIAKLYTQNRKQKQCMQTEQYQFCYETLEVIQ 457  
 DB 860 GVLITMETAMCLIECNQPVYPLDITVETMDQPMVMTQTSQYRFVEALIKYVE 913  
 RESULT 7  
 PTP\_HUMAN STANDARD; PRT; 1337 AA.  
 ID PTP\_HUMAN  
 AC Q12913; Q15255; Q8NEM2;  
 DT 01-NOV-1997 (Rel. 35; Created)  
 DT 10-OCT-2003 (Rel. 42; Last sequence update)  
 DT 10-OCT-2003 (Rel. 42; Last annotation update)  
 DE Protein-tyrosine phosphatase eta precursor (EC 3.1.3.48) (R-PTP-eta)  
 DE (HPP eta) (Protein-tyrosine phosphatase receptor type J) (Density  
 DE enhanced phosphatase-1) (DEP-1) (CD148 antigen).  
 GN PTPR OR DEP1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95024024; PubMed=7937872;  
 RA Oestman A., Yang Q., Tonks N.K.;  
 RT "Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase,  
 RT is enhanced with increasing cell density".  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9680-9684(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95086212; PubMed=7994032;  
 RA Honda H., Inazawa J., Nishida J., Yazaki Y., Hirai H.;  
 RT "Molecular cloning, characterization, and chromosomal localization of  
 RT a novel protein-tyrosine phosphatase, HPP eta".  
 RL Blood 84:4186-4194(1994).  
 RN [3]  
 RP SEQUENCE OF 33-1337 FROM N.A., AND VARIANTS COLON CANCER CYS-214 AND  
 RP PRO-276  
 RC TISSUE=Colon;  
 RX MEDLINE=22084388; PubMed=12089527;



RA Ruitenkamp C.A.L., van Wezel T., Zanon C., Stassen A.P.M., Vloek C.,  
 RA Glikos T., Kious A.M., Tripodis N., Petrakis A., Boerigter L.,  
 RA Groot P.C., Lindeman J., Mooi W.J., Meijer G.A., Scholten G.,  
 RA Dameris H., Paces V., van Zandwijk N., van Ommen G.J.B., Dement P.,  
 RT Pepi is a candidate for the mouse colon-cancer susceptibility locus  
 RT Scl and is frequently deleted in human cancers.",  
 RL Nat. Genet. 31:295-300 (2002).  
 CC -1- FUNCTION: May contribute to the mechanism of contact inhibition of  
 cell growth.  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
 tyrosine + phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- PTM: N- and O-glycosylated.  
 CC -1- DISEASE: Defects in PTPRJ are found in cancers of colon, lung, and  
 breast.  
 CC -1- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.  
 CC -1- SIMILARITY: Contains 5 fibronectin type III domains.  
 CC -1- DATABASE: NAME=PTM; NOTE=CD guide Cdl48 entry;  
 WWW="http://www.ncbi.nlm.nih.gov/ptm/cdl/cdl48.htm".  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: U10886; AAB36687.1; -  
 DR EMBL: D37781; BAA07035.1; -  
 DR EMBL: AF387844; AAM69432.1; -  
 DR EMBL: AF387823; AAM69432.1; JOINED.  
 DR EMBL: AF387824; AAM69432.1; JOINED.  
 DR EMBL: AF387825; AAM69432.1; JOINED.  
 DR EMBL: AF387826; AAM69432.1; JOINED.  
 DR EMBL: AF387827; AAM69432.1; JOINED.  
 DR EMBL: AF387828; AAM69432.1; JOINED.  
 DR EMBL: AF387829; AAM69432.1; JOINED.  
 DR EMBL: AF387830; AAM69432.1; JOINED.  
 DR EMBL: AF387831; AAM69432.1; JOINED.  
 DR EMBL: AF387832; AAM69432.1; JOINED.  
 DR EMBL: AF387833; AAM69432.1; JOINED.  
 DR EMBL: AF387834; AAM69432.1; JOINED.  
 DR EMBL: AF387835; AAM69432.1; JOINED.  
 DR EMBL: AF387836; AAM69432.1; JOINED.  
 DR EMBL: AF387837; AAM69432.1; JOINED.  
 DR EMBL: AF387838; AAM69432.1; JOINED.  
 DR EMBL: AF387839; AAM69432.1; JOINED.  
 DR EMBL: AF387840; AAM69432.1; JOINED.  
 DR EMBL: AF387841; AAM69432.1; JOINED.  
 DR EMBL: AF387842; AAM69432.1; JOINED.  
 DR EMBL: AF387843; AAM69432.1; JOINED.  
 DR PIR: I38670; I38670.  
 DR HSPF: P18052; IYPO.  
 DR GeneW: HGNC:9673; PTPRJ.  
 DR MIM: 600925; -  
 DR GO: GO:0005887; C:intracellular plasma membrane; TAS.  
 DR GO: GO:0005001; P:transmembrane receptor protein tyrosine pho. ; TAS.  
 DR GO: GO:0007267; P:cell-cell signaling; TAS.  
 DR GO: GO:0006470; P:protein amino acid dephosphorylation; TAS.  
 DR GO: GO:000165; P:transmembrane receptor protein tyrosine kin. ; TAS.  
 DR InterPro: IPR008957; FN\_III-like.  
 DR InterPro: IPR003961; FN\_III.  
 DR InterPro: IPR000387; Tyr\_Pp.  
 DR InterPro: IPR000242; Tyr\_Pp.  
 DR Pfam: PF00041; fn3; 6.  
 DR Pfam: PF00102; Y\_Pp\_phosphatase; 1.  
 DR PRINTS: PR00700; PTPRJPHRASE.  
 DR SMART: SM00060; FNS; 1.  
 DR SMART: SM00194; PTPC; 1.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE: PS00056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE: PS00055; TYR\_PHOSPHATASE\_PTP; 1.

KW Signal; Glycoprotein; Transmembrane; Repeat; Hydrolase;  
 KW Disease mutation.  
 FT SIGNAL 1 35  
 FT CHAIN 36 1337  
 FT DOMAIN 36 975  
 FT TRANSMEM 976 996  
 FT DOMAIN 997 1337  
 FT DOMAIN 119 199  
 FT DOMAIN 366 446  
 FT DOMAIN 454 532  
 FT DOMAIN 540 615  
 FT DOMAIN 626 710  
 FT DOMAIN 1065 1337  
 FT ACT SITE 1239 1239  
 FT CARBOHYD 72 72  
 FT CARBOHYD 82 82  
 FT CARBOHYD 93 93  
 FT CARBOHYD 104 104  
 FT CARBOHYD 142 142  
 FT CARBOHYD 172 172  
 FT CARBOHYD 192 192  
 FT CARBOHYD 231 231  
 FT CARBOHYD 258 258  
 FT CARBOHYD 278 278  
 FT CARBOHYD 342 342  
 FT CARBOHYD 351 351  
 FT CARBOHYD 376 376  
 FT CARBOHYD 391 391  
 FT CARBOHYD 396 396  
 FT CARBOHYD 413 413  
 FT CARBOHYD 431 431  
 FT CARBOHYD 501 501  
 FT CARBOHYD 525 525  
 FT CARBOHYD 536 536  
 FT CARBOHYD 582 582  
 FT CARBOHYD 603 603  
 FT CARBOHYD 618 618  
 FT CARBOHYD 628 628  
 FT CARBOHYD 637 637  
 FT CARBOHYD 666 666  
 FT CARBOHYD 669 669  
 FT CARBOHYD 761 761  
 FT CARBOHYD 772 772  
 FT CARBOHYD 784 784  
 FT CARBOHYD 790 790  
 FT CARBOHYD 824 824  
 FT CARBOHYD 910 910  
 FT CARBOHYD 937 937  
 FT VARIANT 214 214  
 FT VARIANT 276 276  
 FT VARIANT 261 261  
 FT CONFLICT 918 929  
 FT SEQUENCE 1337 AA; 145926 WM; E6752521C4B6AF6 CAC64;  
 SQ  
 Query Match 20.0%; Score 487; DB 1; Length 1337;  
 Best Local Similarity 34.9%; Pred. No. 1,5e-26;  
 Matches 110; Conservative 63; Mismatches 114; Indels 28; Gaps 8;  
 Oy 156 SKDTETVSSEKELTQLAQIRPLFNSARABMDCLTKKEELD---ITREPLEEQ 211  
 Db 1003 AKNNVSPS-----QIRP-----KSKLIRVENFAYRKQADBSNGPAEYEDKL 1050  
 Oy 212 MTLPEDDFNSGNTLQNRDKRKYRDLPYDSTRVPLG---KKQYINASYRIYVNEEBYF 267  
 Db 1051 VGISQPKYAAELIAENRCKRYNNVLPYDISRVKLSVQTHSTDYINANYPGYSKDD-- 1108  
 Oy 268 YIATGGPLPETIDPFWQMTLNNCNVTAMITREBCGVTCYSWP-SLSEPLEFHFHSV 327

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DB 1109 FIATGGLPNTLKQFMRVMEKNAVIAITMLTKCEQGTKEBYWP--SKAQQYGDITV 1166
QY 328 FLEFHTVQYFVTRVFOIVKSTGKSCVKHLOFTKPDHGTSPASADPFIRY---VR-YV 383
DB 1167 AMTSEIVLPEWITIRDFVTKNIQTSSSHLRQPHFHSWPDHGVPTDTLLINFRVLVDYM 1226
QY 384 RKSHTTGGLVTHGSGNGVGTGVFCVDVVFSAIEKNSFDMNVTQMKRQCKMIGTKE 443
DB 1227 KQSPESILVHCSGSGVGTGTFALDRLIYQIENMENTVDVGYLVLMKRPILMVGTED 1286
QY 444 QYQFCYEIVLEVLON 458
DB 1287 QYVFLNQCVLDIVRS 1301

RESULT 8
PTNL RAT STANDARD; PRT; 1175 AA.
ID PTNL RAT 062728; 062728;
AC 062728; 062728; (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 42, Last annotation update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase, non-receptor type 21 (BC 3.1.3.48)
DE (Protein-tyrosine phosphatase 2B).
DE PRN21 OR PTP2E.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OK NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2B).
RP STRAIN=Sprague-Dawley;
RC MEDLINE=95104449; PubMed=7805871;
RA L'Abbe D., Banville D., Tong Y., Stocco R., Maason S., Ma S.,
RA Fattus G., Shen S.H.;
RA "Identification of a novel protein tyrosine phosphatase with sequence
RA homology to the cytoskeletal proteins of the band 4.1 family.";
RL FEBS Lett. 356:351-356(1994).
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q62728-1; Sequence=Displayed;
CC Name=2B;
CC IsoId=Q62728-2; Sequence=VSP 000498;
CC -1- TISSUE SPECIFICITY: Particularly abundantly in adrenal glands.
CC -1- SIMILARITY: Contains 1 FERM domain.
CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U17971; AAA62153.1; -
DR EMBL; U17971; AAA62154.1; -
DR PIR; S51005; S51005.
DR HSSP; Q06124; 2SRP.
DR InterPro; IPR000299; Band_4.1.
DR InterPro; IPR000387; TYR_PTPase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00373; Band_41.1.
DR Pfam; PF00102; Y-phosphatase; 1.
DR PRINTS; PR00935; BAND41.
DR PRINTS; PR00700; PRTYPPHTASE.
DR SMART; SM00285; B41.1.
DR SMART; SM00194; PTPc; 1.
DR PROSITE; PS00660; FERM_1; 1.

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DR PROSITE; PS00661; FERM_2; 1.
DR PROSITE; PS50057; FERM_3; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
KM Structural protein; Cytoskeleton; Hydrolyase; Alternative splicing.
FT DOMAIN 23 308 FERM.
FT DOMAIN 922 1175 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 1109 1109 PHOSPHOCYSTEINE INTERMEDIATE
FT ACT_SITE 1109 1109 (BY SIMILARITY).
FT VARSPIC 1 839 Missing (in isoform 2B).
FT FTID=VSP 000498.
SQ SEQUENCE 1175 AA; 133411 MW; 82A684F1C0F5ECF7 CAC64;

Query Match 19.3%; Score 484.5; DB 1; Length 1175;
Best Local Similarity 28.2%; Pred. No. 1.9e-26;
Matches 146; Conservative 69; Mismatches 141; Indels 161; Gaps 17;

QY 81 IPGNKMSENVKD-----SHHSFSDKTELVYPEPLESDTDETVMDVSDRSIRNRNSM 134
DB 677 VFSQKQAGETBQSGGYSHKKSLSDATMLH---SSBDE--DLSDSSKEHAYSE 729
QY 135 DSETAG-----PSKTVSPV-----LSSSRLSKD--TET----- 161
DB 730 PRLTAAPSQQLNYPQASVTPVGPLHPEPKSHVTBPEKAXDISPVHVMETHQPR 789
QY 162 -----SVSEKELTQLAQLRPLFPNSSASAMDC-----NTLO----- 195
DB 790 HGLLTPMSSESLITSGRYR-----ARDSLKRPVSDLSGKNTVGLPLGG 839
QY 196 -KKEBLDIR-----EFLLEQMTLPDDNSGNTL----- 224
DB 840 MKKTRADAKIKIGPKALANGSLSLPLPDEKGVSTRATNDERCKVLEQRLEQGVFT 899
QY 225 -----QNRKRYRDIIPYDSTRVPLAKND---YINASYIRI 259
DB 900 EYERILKKRLVDECSSTARLPENAEERNRFQDVLPYDARVELPTKENNGYINASHIKV 959
QY 260 VNHBEERYATAGPLPETIEDFMQVLENNQVIMITBEICGVYKCYVPLSLKEP 319
DB 960 SVSGIERDIATGPLQNTQCDPMQWMEQVAILIMKVTBEEGSEKSRIRP-----R 1014
QY 320 LBEHPSVPLETFVQYF-----TVRFQIVKSTGKSCVKHLOFTKPDHGTSPAS 372
DB 1015 IGSRHNTVTVGRPKITRRFRDSCGYATGAKKHLITGGERVYMHLYQVDMDEHGGPBD 1074
QY 373 ADFFIKTVRV---KSHITG-----PLVHCSGNGVGTGVFCVDVVFSAIEKNS 421
DB 1075 LKQPLSYLBEIQSVRHHNTSTSEPRSPNPLVHCSGNGVGTGVVLSEITVACLHNEY 1134
QY 422 FDIIMIVTQMKRQCKMIGTKEGYQFCYEIVLEVLON 458
DB 1135 LDIPLRYLRLRQGRMLVQTLISQYTFVRYVLIFLMS 1171

RESULT 9
PTPK HUMAN STANDARD; PRT; 1439 AA.
ID PTPK HUMAN 015262; 014763;
AC 015262; 014763; (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 42, Last annotation update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Receptor-type protein-tyrosine phosphatase kappa precursor
DE (BC 3.1.3.48) (R-PTP-kappa).
GN PTPRK OR PTPK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OK NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RP MEDLINE=96279245; PubMed=8663237;
RA Fuchs M., Mueller T., Lerch M., Ullrich A.;

```

"Association of human protein-tyrosine phosphatase kappa with members of the armadillo family." J. Biol. Chem. 271:16712-16719(1996).

RE SEQUENCE FROM N.A.

RC TISSUE=Forebrain;

RA Yang Y., Gil M.C., Choi B.Y., Park S.H., Pyun K.H., Ha H.;

RT "Molecular cloning and chromosomal localization of a human gene homologous to the murine R-PTP-kappa, a receptor-type protein tyrosine phosphatase";

RL Gene 186:77-82(1997).

CC -1- FUNCTION: Regulation of processes involving cell contact and adhesion such as growth control, tumor invasion, and metastasis. Forms complexes with beta-catenin and gamma-catenin/plakoglobin. Beta-catenin may be a substrate for the catalytic activity of PTP-kappa.

CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein; at adherens junctions.

CC -1- TISSUE SPECIFICITY: High levels in lung, brain and colon; less in liver, pancreas, stomach, kidney, placenta and mammary carcinoma.

CC -1- PTM: This protein undergoes proteolytic processing.

CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

CC -1- SIMILARITY: Contains 4 fibronectin type III domains.

CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.

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CC -----

DR EMBL; Z70660; CA94519.1; -

DR EMBL; L77886; AAC3759.1; -

DR HSSP; P28827; IRPM.

DR Genew; HGNC:9674; PTPRK.

DR MIM; 602545; -

DR GO; GO:0005887; C:integral to plasma membrane; TAS.

DR GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. .; TAS.

DR InterPro; IPR008957; FN-III-like.

DR InterPro; IPR003961; FN-III.

DR InterPro; IPR007110; IG-1-like.

DR InterPro; IPR003599; IG.

DR InterPro; IPR000998; MAM domain.

DR InterPro; IPR000387; TYR phosphatase.

DR InterPro; IPR000242; TYR\_PP.

DR Pfam; PF00041; fn3; 2.

DR Pfam; PF00047; ig; 1.

DR Pfam; PF00629; MAM; 1.

DR Pfam; PF00102; Y\_phosphatase; 2.

DR PRINTS; PR00020; MAMDOMAIN.

DR PRINTS; PR00700; PRTPHPTASE.

DR SMART; SM00060; FN3; 2.

DR SMART; SM00409; IG; 1.

DR SMART; SM00137; MAM; 1.

DR SMART; SM00194; PTPC; 2.

DR PROSITE; PS00835; IG\_LIKE; 1.

DR PROSITE; PS00740; MAM\_1; 1.

DR PROSITE; PS00360; MAM\_2; 1.

DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.

DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 2.

DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.

KM Hydrolyse; Receptor; Glycoprotein; Signal; Transmembrane; Immunoglobulin domain; Repeat.

FT SIGNAL 1 26

FT CHAIN 27 1439

FT DOMAIN 27 752

EXTRACELLULAR (POTENTIAL).

FT TRANSFORM 753 774

FT DOMAIN 775 1439

FT DOMAIN 31 194

FT DOMAIN 196 281

FT DOMAIN 297 384

FT DOMAIN 393 474

FT DOMAIN 494 579

FT DOMAIN 597 680

FT DOMAIN 910 1141

FT DOMAIN 1200 1433

FT ACT\_SITE 1082 1082

FT ACT\_SITE 1376 1376

FT DISULFID 216 270

FT SITE 641 644

FT CARBOHYD 101 101

FT CARBOHYD 140 140

FT CARBOHYD 211 211

FT CARBOHYD 416 416

FT CARBOHYD 424 424

FT CARBOHYD 436 436

FT CARBOHYD 462 462

FT CARBOHYD 552 552

FT CARBOHYD 586 586

FT CARBOHYD 590 590

FT CARBOHYD 607 607

FT CARBOHYD 690 690

FT CONFLICT 9 9

FT CONFLICT 158 158

FT CONFLICT 284 284

FT CONFLICT 422 422

FT CONFLICT 672 672

FT CONFLICT 715 715

FT CONFLICT 732 732

FT CONFLICT 1366 1366

FT CONFLICT 1439 AA; 162087 MW; EED529AF7C9F4451 CRC64;

SO SEQUENCE

Query Match 19.8%; Score 483.5; DB 1; Length 1439;

Best Local Similarity 29.3%; Pred. No. 3e-26;

Matches 135; Conservative 83; Mismatches 182; Indels 61; Gaps 14;

QY 17 EREGSGNINLRSLPSSGQKMTPTKPVQNKIMKYEHLIDIMVFLIKTIYVNFELM 76

DB 718 EKETKQCVAVIAVKAATSEBEVIPPDAKQIDRVKLAGISAGILVILLIVLIVK-- 775

QY 77 KKKLIKGNK--MNSNVKXSHL-----SPSDKELVPEPLSDDEFTVWDSLSRY 129

DB 776 KSKLAKKRDAMNTRQENTHVNAMDRSYADOSTLHAEDPLSI---TMDQHNFSKY 831

QY 130 RANSMDETAGPKTVSPVLSSGSSRLKDTETSVSEKELTOLAQIIBPLIFNSASRGA-MR 188

DB 832 ENHSATFES-----SRLLDVPRVLCGEBTSFY-----QTQLHPAI-----RVADLL 873

QY 189 DCANTLQKKEELDIIEPLEBQMTLPDDPNSGNTL-----QNRDKRYRDIIPYDS 240

DB 874 QHINIKTSDSYGPKREY-----ESFEBQSSMDVAKQDQNPANRKGITAIYDH 924

QY 241 TRVPL-----GKKQDYINASYIRIVNHEBEFYIAQGPLPFIEDFWQVVLNNCNVIA 295

DB 925 SRVILQPEVEDPSSDIDNNYID--GYQPSHIAIAQGPVHEVYDFWEMIMQEOSACIV 982

QY 296 MTRREIEGVYIKYISWPIISLKEPLFEHFSVLEFPHVQYTVAVPQVVKSTGSQC 355

DB 983 MVTNLVEVGKVKYKVPDQTEVYGPKYLCVMEBL--AEVTVPTFLRGNVNEIRZ 1039

QY 356 VKHLQFTKMPDHGTPASADFFIKYRVRKSH--ITGPLVHCSAGVGRGVICVDVF 413

DB 1040 VKQPHFTGPDHGVPHATGLLSFIRKVLNSPPSAGPIVHESAGRGCTIVDIML 1099

QY 414 SAIEKNSPDIMNIVTOMERKQRCGMITKEQYQFCREIVLE 454

DB 1100 DMAEREGVDVIVCVALRSRRINWVQTEBOYIFIDDAILE 1140

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RESULT 10
PRTT HUMAN STANDARD; PRT: 1463 AA.
ID MEDLINE=22730717; PubMed=11814386;
AC 014522; 043655; 075664; 09BR24; 09BR28; 0910Y8; 09NTL1; 09NT72;
AC 09UBD2; 09NU17;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Receptor-type protein-tyrosine phosphatase T precursor (EC 3.1.3.48)
DE (R-PTP-T) (RPTP-tho).
DE PRTT OR KIAA0283.
CN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP MEDLINE=98267260; PubMed=9602027;
RX MEDLINE=98267260; PubMed=9602027;
RA McAndrew P.E., Frostholm A., White R.A., Rotter A., Burghes A.H.M.;
RT "Identification and characterization of RPTP tho, a novel RPTP
RT mu/Kappa-like receptor protein tyrosine phosphatase whose expression
RT is restricted to the central nervous system."
RL Brain Res. Mol. Brain Res. 56:9-21(1998).
RN [2]
RP MEDLINE=98267260; PubMed=9602027;
RX MEDLINE=98267260; PubMed=9602027;
RA McAndrew P.E., Frostholm A., White R.A., Rotter A., Burghes A.H.M.;
RT "Identification and characterization of RPTP tho, a novel RPTP
RT mu/Kappa-like receptor protein tyrosine phosphatase whose expression
RT is restricted to the central nervous system."
RL Brain Res. Mol. Brain Res. 56:9-21(1998).
RN [3]
RP MEDLINE=98267260; PubMed=9602027;
RX MEDLINE=98267260; PubMed=9602027;
RA McAndrew P.E., Frostholm A., White R.A., Rotter A., Burghes A.H.M.;
RT "Identification and characterization of RPTP tho, a novel RPTP
RT mu/Kappa-like receptor protein tyrosine phosphatase whose expression
RT is restricted to the central nervous system."
RL Brain Res. Mol. Brain Res. 56:9-21(1998).
RN [4]
RP MEDLINE=98267260; PubMed=9602027;
RX MEDLINE=98267260; PubMed=9602027;
RA McAndrew P.E., Frostholm A., White R.A., Rotter A., Burghes A.H.M.;
RT "Identification and characterization of RPTP tho, a novel RPTP
RT mu/Kappa-like receptor protein tyrosine phosphatase whose expression
RT is restricted to the central nervous system."
RL Brain Res. Mol. Brain Res. 56:9-21(1998).
RN [5]
RP MEDLINE=98267260; PubMed=9602027;
RX MEDLINE=98267260; PubMed=9602027;
RA McAndrew P.E., Frostholm A., White R.A., Rotter A., Burghes A.H.M.;
RT "Identification and characterization of RPTP tho, a novel RPTP
RT mu/Kappa-like receptor protein tyrosine phosphatase whose expression
RT is restricted to the central nervous system."
RL Brain Res. Mol. Brain Res. 56:9-21(1998).

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FT	DOMAIN	788	1463	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	30	191	NAM
FT	DOMAIN	193	284	IG-LIKE C2-TYPE.
FT	DOMAIN	289	374	FIBRONECTIN TYPE-III 1.
FT	DOMAIN	386	480	FIBRONECTIN TYPE-III 2.
FT	DOMAIN	481	584	FIBRONECTIN TYPE-III 3.
FT	DOMAIN	589	726	FIBRONECTIN TYPE-III 4.
FT	DOMAIN	911	1165	PROTEIN-TYROSINE PHOSPHATASE 1.
FT	DOMAIN	1197	1459	PROTEIN-TYROSINE PHOSPHATASE 2.
FT	ACT_SITE	1106	1106	PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).
FT	ACT_SITE	1400	1400	PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).
FT	DISULFID	213	267	POTENTIAL.
FT	CARBOHYD	58	58	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	78	78	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	98	98	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	137	137	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	208	208	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	421	421	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	510	510	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	547	547	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	601	601	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	654	654	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	684	684	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VASSP-LIC	726	744	Missing (in isoform 2).
FT	CONFLICT	29	29	/FTID=VSP_007802.
FT	CONFLICT	60	60	P -> A (IN REF. 3).
FT	CONFLICT	375	375	T -> W (IN REF. 1).
FT	CONFLICT	801	803	A -> P (IN REF. 1).
FT	CONFLICT	889	889	MISSING (IN REF. 1).
FT	CONFLICT	889	889	L -> P (IN REF. 1).
SEQ	SEQUENCE	1463 AA:	164275	MM; BE4B4B83B8A4017 CRCA4;

Query Match	19.7%;	Score 481.5;	DB 1;	Length 1463;
Best Local Similarity	27.9%;	Pred. No. 4.2e-26;		
Matches 139;	Conservative 75;	Mismatches 163;	Indels 121;	Gaps 17

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QY 25 :NLNRSLSSSCOMPTKPY-----QNNLKKVECHLDI-----LAWFLLI 65
Db 720 VRLAKAMGSAQVTPGTPLCLTTTGASQSNNTYPEPQOVNTYKMGVIAGLMFLII 779
QY 66 KTIWYVFEKLMGKKLI FGNKNSENVKSBHLSFSDXYELVYPEPLESDTETVMDVDR 125
Db 780 -----LLGYMLTIKRRBNAYSYSY-----LSQR 803
QY 126 SLNRNNSMDSPTAGPSKTVSPVLS-----GSSRLSKOTE--TSVSEKL 168
Db 804 KLAKKQKETOS--GAOREMPVASADKETTYTLASRNDEGSSSSODVNGCTDSRGEL 860
QY 169 TO--LAQIRPL-----IFNSSARSAMRDCMLNTLQK-----KEELDI 203
Db 861 SQPLTITQTHPYRTCDPVMSYPRDQFOAIRVA--DLLQHTQMRGQGYGFKSEYAL 918
QY 204 REFELEGMTLPBDNNSGNTLONRDNKRYROLIPLPDSRYPL-----GKNKYIANSYR 258
Db 919 PEGQTASMDTAKED-----ERNKKNRGNTIISYDHSVRLVLTGDGPHSDIYNANTYI 971
QY 259 IYNHEEVEFYIATQGPPELTIEDFQOMYLENNCNVMIAMTBEIECGVIKCYSWYELSK 318
Db 972 --GYHRPHYIATQGPQOETVWDPFMRMIQENSASIVMTNLVVERGVKCVATWPDDEEV 1022
QY 319 PLEFHFVSVELETFRHYQFYTVRVRQIYKKSQSGKQCVCHLOFTKMRPHGTASADPFIK 378
Db 1030 YGDIR--VTLTETEPLEAV--VIRTTVOKKGYHEIRELCEFFHTSPDHGVCYANTGLG 1088
QY 379 YRVYR--KSHITGELVHCSAGVARTGVFICVDVVPASILEKXYSFDINVIYTONKORC 436
Db 1087 FVRQYKFLNRPBAGRIVVHCSAGAGRTGCFIADITMLDAENEGVYDIFNCRVREPAQGV 1146
QY 437 GMIOTKEQOQCYCYVILE 454
Db 1147 NLVQTEEQVVEVHADILE 1164

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RESULT 11			
PTPD_HUMAN	STANDARD;	PTI:	1912 AA.
ID	PTPD_HUMAN		
AC	P23468;		
DT	01-NOV-1991 (Rel. 20, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DT	Protein-tyrosine phosphatase delta precursor (BC 3.1.3.48) (R-PTP-delta).		
DE	Protein-tyrosine phosphatase delta precursor (BC 3.1.3.48) (R-PTP-delta).		
GN	PTPRD.		
OS	Homo sapiens (Human).		
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_Taxid:9606;		
RN	[1]		
RP	SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-1178.		
RX	MEDLINE=95204468; PubMed=7896816;		
RA	Pulido R., Knueger N.X., Serra-Pages C., Saito H., Streuli M.;		
RT	"Molecular characterization of the human transmembrane protein-tyrosine phosphatase delta. Evidence for tissue-specific expression of alternative human transmembrane protein-tyrosine phosphatase delta isoforms.";		
RT	J. Biol. Chem. 270:6722-6728(1995).		
RL	[2]		
RN	SEQUENCE OF 390-1912 FROM N.A.		
RP	TISSUE=Placenta;		
RX	MEDLINE=9106016; PubMed=2170109;		
RA	Knueger N.X., Streuli M., Saito H.;		
RT	"Structural diversity and evolution of human receptor-like protein tyrosine phosphatases.";		
RT	EMBO J. 9:3241-3252(1990).		
RL	-1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.		
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.		
CC	-1- ALTERNATIVE PRODUCTS:		
CC	Event=Alternative splicing; Named isoforms=3;		
CC	Comment=Additional isoforms seem to exist;		
CC	Name=1;		
CC	Isoid=P23468-1; Sequence=Displayed;		
CC	Name=2; Synonyms=Kidney;		
CC	Isoid=P23468-2; Sequence=VSP_005147, VSP_005148, VSP_005149;		
CC	Name=3; Synonyms=Petal brain;		
CC	Isoid=P23468-3; Sequence=VSP_005150;		
CC	-1- FROM THE TRANSMEMBRANE SEGMENT.		
CC	-1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.		
CC	-1- SIMILARITY: Contains 8 fibronectin type III domains.		
CC	-1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).		
DR	EMBL; L38929; AAC41749.1; -		
DR	EMBL; X54133; CAA38068.1; -		
DR	PIR; A56178; A56178.		
DR	HSSP; P18052; 1YPO.		
DR	Genew; HGNC:3668; PTPRD.		
DR	MLN; E01598; -		
DR	GO; GO:0005887; C: integral to plasma membrane; TAS.		
DR	GO; GO:0005001; P: transmembrane receptor protein tyrosine pho. . .; TAS.		
DR	GO; GO:0006470; P: protein amino acid dephosphorylation; TAS.		
DR	GO; GO:0007185; P: transmembrane receptor protein tyrosine pho. . .; TAS.		
DR	InterPro; IPR006957; FN_III-like.		
DR	InterPro; IPR003961; FN_III.		
DR	InterPro; IPR003962; FNIII_subd.		
DR	InterPro; IPR007110; Ig-like.		

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DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR000387; Tyr_phosphatase.
DR InterPro: IPR000242; Tyr_Pp.
DR Pfam: PF00044; fn3; 8.
DR Pfam: PF00047; Ig; 3.
DR Pfam: PF0102; Y_phosphatase; 2.
DR PRINTS: PR00014; PTYPHPTASE.
DR SMART: SM00060; FN3; 8.
DR SMART: SM00408; IGC2; 2.
DR SMART: SM00194; PTPC; 2.
DR PROSITE: PS00835; IG_LIKE; 3.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS00056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS00055; TYR_PHOSPHATASE_PTP; 2.
DR Hydrolyase; Receptor; Glycoprotein; Signal; Transmembrane; Repeat;
KW Immunoglobulin domain; Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 1 1912
FT DOMAIN 21 1265
FT TRANSMEM 1266 1290
FT DOMAIN 1291 1912
FT DOMAIN 124 114
FT DOMAIN 126 224
FT DOMAIN 236 318
FT DOMAIN 320 414
FT DOMAIN 417 513
FT DOMAIN 516 606
FT DOMAIN 609 708
FT DOMAIN 711 822
FT DOMAIN 825 916
FT DOMAIN 918 1017
FT DOMAIN 1020 1137
FT DOMAIN 1375 1618
FT ACT_SITE 1519 1912
FT ACT_SITE 1553 1553
FT ACT_SITE 1844 1844
FT SITE 1175 1178
FT CARBOHYD 254 254
FT CARBOHYD 299 299
FT CARBOHYD 724 724
FT CARBOHYD 832 832
FT VARSPLIC 181 189
FT VARSPLIC 226 229
FT VARSPLIC 775 783
FT VARSPLIC 609 1137
FT MUTAGEN 1178 1178
FT SEQUENCE 1912 AA; 214755 MW; 3A88CED32182E26 CRC64;
Query Match 19.7%; Score 481.5; DB 1; Length 1912;
Best Local Similarity 40.2%; Pred. No. 6e-26;
Matches 107; Conservative 45; Mismatches 93; Indels 21; Gaps 7;

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Db 1819 GFIDFGQVHTKEQFQDQDPISVHSGAGVGRGVFTTSLVIERMYBGVVDIFQTVKM 1878
Oy 431 MRKRCGMIOETKEQYQCYEIVLSEVL 456
Db 1879 LRTQRPANVOTEDQYQSYRAALEYL 1904

RESULT 12
PTNL_MOUSE STANDARD; PRT; 1176 AA.
AC 062136;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 21 (BC 3.1.3.48)
DE (Protein-tyrosine phosphatase PTP-RL10).
GN PTPN21.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Liver;
RX MEDLINE=9514043; PubMed=7836537;
RA Higashitani H., Arai S., Furutani M., Imamura M., Kaneko Y.,
RA Takemawa J., Nakayama H., Fujita J.,
RT "Enhanced expression of multiple protein tyrosine phosphatases in the
RT regenerating mouse liver: isolation of PTP-RL10, a novel cytoplasmic-
RT type phosphatase with sequence homology to cytoskeletal protein
RT 4.1."
RL Oncogene 10:407-414(1995).
CC -1- FUNCTION: May be involved in the regulation of growth and
CC differentiation of liver cells.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -1- TISSUE SPECIFICITY: Liver.
CC -1- SIMILARITY: Contains 1 PFM domain.
CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
CC -----
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CC -----
DR EMBL: D37801; BAA07053.1; -.
DR PIR: I58345; I58345.
DR HSP: P29350; IGWZ.
DR MGI: MGI:1344406; Ptpn21.
DR InterPro: IPR000299; Band 4.1.
DR InterPro: IPR000387; Tyr_phosphatase.
DR InterPro: IPR000242; Tyr_Pp.
DR Pfam: PF00373; Band_41; 1.
DR Pfam: PF00102; Y_phosphatase; 1.
DR PRINTS: PR00935; BAND41.
DR PRINTS: PR00700; PTYPHPTASE.
DR SMART: SM00295; B41; 1.
DR SMART: SM00194; PTPC; 1.
DR PROSITE: PS00660; FERM_1; 1.
DR PROSITE: PS00661; FERM_2; 1.
DR PROSITE: PS00057; FERM_3; 1.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS00055; TYR_PHOSPHATASE_PTP; 1.
DR PROSITE: PS00056; TYR_PHOSPHATASE_2; 1.
KM Structural protein; Cytoskeleton; Hydrolyase.
FT DOMAIN 923 308
FT DOMAIN 1176 1176
FT ACT_SITE 1110 1110
FT ACT_SITE 1110 1110
FT PROTEIN-TYROSINE PHOSPHATASE.
FT PHOSPHOCYSTEINE INTERMEDIATE
FT (BY SIMILARITY).

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FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 415 415 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 435 435 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 551 551 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 585 585 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 589 589 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 689 689 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1457 AA; 154185 MW; 19D4B99B73CE8605 CRC64;

Query March 19.6%; Score 477.5; DB 1; Length 1457;
Best Local Similarity 29.6%; Pred. No. 8e-26;
Matches 129; Conservative 72; Mismatches 158; Indels 77; Gaps 13;

QY 59 LMVLLIYIYNYFKMKGLIFGNK--NNSENVKSHL-----SPSDKYLVEPEPL 111
DB 760 ILVFIILLVIVIVK--KSKLAKKRDAMGNTROEMTHVNMADRSYADOSTLHADPL 817
QY 112 ESDDEIYWDVSDSLRRNMSDETGPEKTVSPVLSGSSKSLKOTETSVSKEELT-- 169
DB 818 S-----LTFMDQHNFSPLPNDPLVPTAVLDENHSATAESSRLLDVP 859
QY 170 -----QLAQIRPLIFNSASRSA-MEDCLNTLOKKELDIREFLELQWTLPPD 217
DB 860 RYLCEGTESPYQTQGLHAI-----RVADLIQHNKMTSISYGFKEEY-----ES 905
QY 218 FNSGNTL-----QNDKRRYDILYDSTRVPL-----GRNKDYINASYIRIVNHEE 264
DB 906 FFEQGSASMDYAKDQNRKAKRYGNIILAYDHSRVLQVEVDPSDDYINANYIDIMLYRD 965
QY 265 EY----FYIATQGPLERTIEDFMQVLENNCNVIAITREIECGVICYSWYPSLSKPL 320
DB 966 GYRPSHYIATQGFHEVTVDFMRKWSQSACTVMTNLVEARVCKYKWPDPTEYVG 1025
QY 321 EFHFSVPLETFHYQVFTVAVFOIVKKSQCVKRLQPTKMPDHTSPASADPFIKYV 380
DB 1026 DFKVTCVMEPL---AEYVATFTLIRGMYRIEVRQFHTGMPDGVPHVATGLISFI 1082
QY 381 RYVKRSH--ITGELLVHSAGVGRGVICVDVVFSAIEKRYSDINMIVQNRKQCGM 438
DB 1083 RRVKLSNPASAGPIVHCSAAGRTGYIVIDIMLDMABRGVVDVYNCVYALSRIRM 1142
QY 439 IQTEKQYQFCYEIVLE 454
DB 1143 VQTEQYIFHIDALE 1158

RESULT 14
PRTJ MOUSE STANDARD; PRT; 1238 AA.
AC 064455;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase eta precursor (EC 3.1.3.48) (R-PTP-eta)
DE (HPTP beta-like tyrosine phosphatase) (Protein-tyrosine phosphatase
DE receptor type J) (Susceptibility to colon cancer-1).
GN PTPRJ OR BYP OR SCC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MRL-LPR/LPR;
RX MEDLINE=96140699; PubMed=8549806;
RA Yamamoto S., Matsuda S., Matsuda Y., Saitoh T., Ohsugi M.,
RA Kuramochi T.,
RA "Molecular cloning and characterization of ByP, a murine
RT receptor-type tyrosine phosphatase similar to human DEP-1.";
RL FEBS Lett. 378:7-14(1996).

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CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in every tissue examined.
CC -1- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.
CC -1- SIMILARITY: Contains 6 fibronectin type III domains.
CC -----
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CC -----
DR EMBL; D45212; BA08146.1; -.
DR PIR; S68700; S68700.
DR HSP; P18052; IYFO.
DR MGD; MGI:104574; Ptdr1.
DR GO; GO:0007507; P-heart development; IMP.
DR GO; GO:0001570; P-vasculogenesis; IMP.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR00387; Tyr_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 6.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPPHASE.
DR SMART; SM00060; FN3; 6.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
DR Signal; glycoprotein; Transmembrane; Repeat; Hydrolase.
KT Signal; 1
FT CHAIN 1 28
FT 29 1238
FT 29 876
FT 877 897
FT TRANSHEM 898 1238
FT DOMAIN 898 1112
FT DOMAIN 121 260
FT DOMAIN 268 348
FT DOMAIN 356 434
FT DOMAIN 442 518
FT DOMAIN 529 608
FT DOMAIN 966 1238
FT ACT_SITE 1140 1140
FT CARBOHYD 62 62
FT CARBOHYD 78 78
FT CARBOHYD 85 85
FT CARBOHYD 90 90
FT CARBOHYD 110 110
FT CARBOHYD 114 114
FT CARBOHYD 145 145
FT CARBOHYD 164 164
FT CARBOHYD 173 173
FT CARBOHYD 182 182
FT CARBOHYD 198 198
FT CARBOHYD 207 207
FT CARBOHYD 244 244
FT CARBOHYD 253 253
FT CARBOHYD 267 267
FT CARBOHYD 278 278
FT CARBOHYD 313 313
FT CARBOHYD 317 317
FT CARBOHYD 333 333
FT CARBOHYD 366 366
FT CARBOHYD 379 379
FT CARBOHYD 398 398
FT CARBOHYD 403 403
FT CARBOHYD 437 437
FT CARBOHYD 452 452

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## OM protein - protein search, using sw model

Run on: June 18, 2004, 19:35:53 ; Search time 46 Seconds  
(without alignments)  
3175.759 Million cell updates/sec

Title: US-09-095-478a-6

Perfect score: 2439  
Sequence: 1 MSPPRYRGRKGRNDDEEG.....QYCYEIVLEVLQNIALLY 463

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP archaea:\*  
2: SP bacteria:\*  
3: SP fungi:\*  
4: SP human:\*  
5: SP invertebrate:\*  
6: SP mammal:\*  
7: SP tbc:\*  
8: SP organelle:\*  
9: SP phage:\*  
10: SP plant:\*  
11: SP rodent:\*  
12: SP virus:\*  
13: SP vertebrate:\*  
14: SP unclassified:\*  
15: SP viirus:\*  
16: SP bacteriaph:\*  
17: SP archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2212.5	90.7	426 11 055082	055082 mus musculu
2	1306	53.5	398 4 Q9Y406	Q9Y406 homo sapien
3	653	26.8	2460 11 064512	064512 mus musculu
4	651	26.7	2484 6 028006	028006 bos taurus
5	502	20.6	926 11 09W122	09W122 mus musculu
6	500	20.5	292 4 08N453	08N453 homo sapien
7	497	20.4	2051 5 044328	044328 hirtudo medl
8	496.5	20.4	615 13 091A18	091A18 xenopus lae
9	496.5	20.4	849 11 091J18	091J18 mus musculu
10	493.5	20.2	468 13 091B10	091B10 potamoctryo
11	493.5	20.2	857 13 090Y14	090Y14 brachydano
12	491.5	20.2	468 13 091B12	091B12 potamoctryo
13	491.5	20.2	832 13 090Y17	090Y17 gallus galli
14	490.5	20.1	1502 4 Q9UM81	Q9UM81 homo sapien
15	489.5	20.1	749 11 08R169	08R169 mus musculu
16	489.5	20.1	1254 11 08YB10	08YB10 mus musculu

17	488.5	20.0	597 13 Q91871	Q91871 xenopus lae
18	487	20.0	758 11 Q7TM61	Q7TM61 mus musculu
19	486	19.9	468 13 Q9N106	Q9N106 eptatretus
20	484.5	19.9	1896 13 Q91AJ1	Q91AJ1 xenopus lae
21	484	19.8	1156 5 Q21214	Q21214 caenorhabdi
22	484	19.8	1222 13 Q8MY44	Q8MY44 eptatretus
23	483	19.8	1100 13 Q8MY45	Q8MY45 eptatretus
24	483	19.8	1187 13 Q8MY42	Q8MY42 eptatretus
25	483	19.8	1202 13 Q8MY43	Q8MY43 eptatretus
26	483	19.8	1092 13 Q90815	Q90815 gallus galli
27	480	19.7	694 13 Q7ZYX2	Q7ZYX2 xenopus lae
28	479.5	19.7	469 13 Q9N108	Q9N108 eptatretus
29	479.5	19.7	1440 4 Q86WJ2	Q86WJ2 homo sapien
30	478.5	19.6	469 5 Q9N111	Q9N111 brachioctro
31	478.5	19.6	907 13 Q8MY41	Q8MY41 eptatretus
32	478	19.6	1338 11 Q8K302	Q8K302 mus musculu
33	477	19.6	1501 11 Q7T117	Q7T117 mus musculu
34	476	19.5	1216 11 Q62884	Q62884 rattus norv
35	476	19.5	1406 13 Q9W6V5	Q9W6V5 gallus galli
36	476	19.5	1501 11 Q9QW00	Q9QW00 rattus sp.
37	476	19.5	1863 11 Q64505	Q64505 rattus norv
38	475.5	19.5	1998 11 Q8C1W2	Q8C1W2 mus musculu
39	475.5	19.5	2271 13 Q91909	Q91909 xenopus lae
40	475	19.5	361 11 Q61373	Q61373 mus musculu
41	475	19.5	694 13 Q91870	Q91870 xenopus lae
42	474.5	19.5	1195 13 Q9PUM2	Q9PUM2 xenopus lae
43	474.5	19.5	1904 11 Q64699	Q64699 mus musculu
44	473.5	19.4	1102 11 Q80VW7	Q80VW7 mus musculu
45	473	19.4	336 11 Q9QW07	Q9QW07 mus musculu

## ALIGNMENTS

## RESULT 1

055082 PRELIMINARY; PRT; 426 AA.

AC 055082;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Protein-tyrosine-phosphatase (EC 3.1.3.48).  
GN PTPN20.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RX MEDLINE=98070510; PubMed=9407093;  
RA Ohsugi M., Kuramochi S., Matsuda S., Yamamoto T.;  
RT "Molecular cloning and characterization of a novel cytoplasmic  
RT protein-tyrosine phosphatase that is specifically expressed in  
RT spermatocytes.";  
RL J. Biol. Chem. 272:33092-33099(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RX MEDLINE=22354683; PubMed=12466811;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573 (2002).  
DR EMBL; D64141; BAA23761.1; -  
DR EMBL; AK029493; BAC26476.1; -  
DR HSSP; Q06124; ZSHP.  
DR MGD; MGI:1196295; Ptpn20.  
DR GO; GO:0016887; F:hydrolase activity; IEA.  
DR GO; GO:0004227; F:phosphatase activity; IEA.  
DR GO; GO:0006707; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR000387; Tyr\_phosphatase.

DR InterPro: IP000242; Tyr\_PP.  
 DR Pfam: PF00102; Y\_phosphatase; 1.  
 DR PRINTS: PR00700; PRTPPHPTASE.  
 DR SMART: SM00194; PTPC; 1.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE: PS50056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE: PS50055; TYR\_PHOSPHATASE\_PTP; 1.  
 DR HydroLase.  
 SQ SEQUENCE 426 AA; 4918 MM; 2835EB13379502F4 CRC64;

Query Match 90.7%; Score 2212.5; DB 11; Length 426;  
 Best Local Similarity 92.0%; Pred. No. 1.9e-163;  
 Matches 426; Conservative 0; Mismatches 0; Indels 37; Gaps 1;

QY 1 MSSPRKVGKGTGRNDDEEGNSGNLNLNSLPSSSQKMTPTKPVQNTKMLKYEELHLLM 60  
 DB 1 MSSPRKVGKGTGRNDDEEGNSGNLNLNSLPSSSQKMTPTKPVQNTKMLKYEELHLLM 43  
 QY 61 VFLLIKTIWVVFVKLMKCKLIFGNKNSENVKPSHHLSFSDKYEIVYPEPLESDTDETW 120  
 DB 44 -----IFGNKNSENVKPSHHLSFSDKYEIVYPEPLESDTDETW 83  
 QY 121 DVSDRSLRNWNSDSETPAGSKTVSPVLSGSSRLSKDTEVSSEKELTQLAQIRPLIFN 180  
 DB 84 DVSDRSLRNWNSDSETPAGSKTVSPVLSGSSRLSKDTEVSSEKELTQLAQIRPLIFN 143  
 QY 181 SSASASAMDCIANTLOKKEELIIRFLELEQMTLPDDPNSGNTQNRDKRRYRDLFYDS 240  
 DB 144 SSASASAMDCIANTLOKKEELIIRFLELEQMTLPDDPNSGNTQNRDKRRYRDLFYDS 203  
 QY 241 TRVPLGKKQKQYINASYIRIVNHEEYFYIATQGLPETIEDFMQVLENNCNVAMITRE 300  
 DB 264 TRVPLGKKQKQYINASYIRIVNHEEYFYIATQGLPETIEDFMQVLENNCNVAMITRE 263  
 QY 301 IECGVIKCYSWPISLKEPLFEHPVSFLETHNTQFTFVFOIVKKSSTGSCCVKHLQ 360  
 DB 264 IECGVIKCYSWPISLKEPLFEHPVSFLETHNTQFTFVFOIVKKSSTGSCCVKHLQ 323  
 QY 361 FTKMPDHGTSPASADPFICYVYVYRKSHITGPLVHCSAGVGTGVPICVDVVFSAIKNY 420  
 DB 324 FTKMPDHGTSPASADPFICYVYVYRKSHITGPLVHCSAGVGTGVPICVDVVFSAIKNY 383  
 QY 421 SFDINKIVTQMKORCGKIQTKEQYQFCYEIVLEVLQNTLALY 463  
 DB 384 SFDINKIVTQMKORCGKIQTKEQYQFCYEIVLEVLQNTLALY 426

## RESULT 2

ID Q9Y406 PRELIMINARY; PRT; 398 AA.  
 AC Q9Y406;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 GN DKFPP566K0524.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Anstorg W., Wilkner U., Mewes H.W., Gassenhuber U., Wiemann S.,  
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL050040; CAB3248.1; -  
 DR PIR: T08716; T08716.  
 DR HSSP: Q06124; 2SHR.  
 DR GO: GO:0016787; F:Hydrolase activity; IEA.  
 DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
 DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro: IP000387; Tyr\_phosphatase.  
 DR InterPro: IP000242; Tyr\_PP.

DR Pfam: PF00102; Y\_phosphatase; 1.  
 DR PRINTS: PR00700; PRTPPHPTASE.  
 DR SMART: SM00194; PTPC; 1.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE: PS50056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE: PS50055; TYR\_PHOSPHATASE\_PTP; 1.  
 DR HydroLase.  
 SQ SEQUENCE 398 AA; 45690 MM; 857AAD03747870A2 CRC64;

Query Match 53.5%; Score 1306; DB 4; Length 398;  
 Best Local Similarity 65.8%; Pred. No. 4.1e-93;  
 Matches 252; Conservative 48; Mismatches 75; Indels 8; Gaps 2;

QY 81 IFGNKNSENVKPSHHLSFSDKYEIVYPEPLESDTDETWVSDRSLRNWNSDSETPAG 140  
 DB 22 VFENKNSENVKPSHHLSFSDKYEIVYPEPLESDTDETWVSDRSLRNWNSDSETPAG 81  
 QY 141 PSKTVSPVLSGSSRLSKDTEVSSEKELTQLAQIRPLIFNSSASAMDCIANTLOKKE 159  
 DB 82 PSQALSPPLS-----DTRKTVSEGLDQLAQIRPLIFNFBQTLAKDLKLEKTA 134  
 QY 200 LDIIRFLELEQMTLPDDPNSGNTQNRDKRRYRDLFYDSTRVPLGKKQKQYINASYIRI 259  
 DB 135 YDIHQEPMLLEKNLPGFYSYSGNQPENREKNRYRDLFYDSTRVPLGKKQKQYINASYIRI 194  
 QY 260 VNHREYFYIATQGLPETIEDFMQVLENNCNVAMITREIECGVTKCYSTPISLKEP 319  
 DB 195 VNHREYFYIATQGLPETIEDFMQVLENNCNVAMITREIECGVTKCYSTPISLKEP 254  
 QY 320 LIEFHVSFLETHNTQFTFVFOIVKKSSTGSCCVKHLQFTKMPDHGTSPASADPFIKY 379  
 DB 255 LIEKHFRVLENTQIQTIFIMFYVEKSTGSHSVKQLQFTKMPDHGTSPASADPFIKY 314  
 QY 380 VHYRKSHITGPLVHCSAGVGTGVPICVDVVFSAIKNYGSDINKIVTQMKORCGK 439  
 DB 315 IRYARKSHITGPMVHVCAGIGTGVFLCVDVVFCAIVDCSFNMDIVAQMKRQSSGMV 374  
 QY 440 QTKEQYQFCYEIVLEVLQNTLAL 462  
 DB 375 QTKEQYHFCYDIVLEVLKLLTL 397

## RESULT 3

ID Q64512 PRELIMINARY; PRT; 2460 AA.  
 AC Q64512; Q64512; Q64512; Q64512;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Protein-tyrosine phosphatase, NONRECEPTOR-type, 13 (EC 3.1.3.48)  
 DE (Protein-tyrosine-phosphatase) (Phosphotyrosine phosphatase) (PTPase)  
 DE (PTP36).  
 GN PTPN13 OR PTP14.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=SKIN;  
 RX MEDLINE=96340953; PubMed=8749712;  
 RA Hendricks W., Schepens J., Baechner D., Rijse J., Zeeuwen P.,  
 RT Zechner U., Hameister H., Wieringa B.;  
 RT "Molecular cloning of a mouse epithelial protein-tyrosine phosphatase  
 with similarities to submembranous proteins";  
 RL J. Cell. Biochem. 59:418-430(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DEA/2;  
 RX MEDLINE=95145716; PubMed=7843407;  
 RA Chida D., Kume T., Mukoyama Y., Tabata S., Nomura N., Thomas M.,

RA Matanabe T., Oishi M.;  
 RT "Characterization of a protein tyrosine phosphatase (RIP) expressed at  
 RT a very early stage of differentiation in both mouse erythroleukemia  
 RT and embryonal carcinoma cells.";  
 RT FEBS Lett. 358:233-239(1995).  
 RN [3]  
 RN SEQUENCE OF 1105-2460 FROM N.A.  
 RC STRAIN=CB.17 SCID; TISSUE=THYMUS;  
 RX MEDLINE=94354845; PubMed=8074693;  
 RA Sawada M., Ogata M., Fujino Y., Hamacka T.;  
 RT "cDNA cloning of a novel protein tyrosine phosphatase with homology to  
 RT cytoskeletal protein 4.1 and its expression in T-lymphocyte cells.";  
 RL Biochem. Biophys. Res. Commun. 203:479-484(1994).  
 RN [4]  
 RN SEQUENCE OF 2266-2372 FROM N.A.  
 RC STRAIN=BALB/C; TISSUE=BRN;  
 RX MEDLINE=95134232; PubMed=7832766;  
 RA Hendriks W., Schepens J., Brugman C., Zeeuwen P., Wieringa B.;  
 RT "A novel receptor-type protein tyrosine phosphatase with a single  
 RT catalytic domain is specifically expressed in mouse brain.";  
 RL Biochem. J. 305:499-504(1995).  
 CC -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O = PROTEIN  
 CC TYROSINE + PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN KIDNEY AND, TO A  
 CC LESSER EXTENT, IN LUNG, HEART, BRAIN AND TESTIS.  
 CC -1- SIMILARITY: CONTAINS A DOMAIN FOUND IN BAND 4.1, EZRIN, MOESIN,  
 CC RADIXIN, AND TALIN.  
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-  
 CC TYROSINE PHOSPHATASE FAMILY.  
 DR EMBL: Z32740; CAAB3650.1; -;  
 DR EMBL: D83966; BAA12158.1; -;  
 DR EMBL: D28529; BAA05885.1; -;  
 DR EMBL: Z23059; CAA80594.1; -;  
 DR PIR: S40290; S40290.  
 DR PDB: 1GMT; 08-MAR-02.  
 DR MED: MGI:103293; Ppnl3.  
 DR GO: GO:0005856; C:cytoskeleton; IEA.  
 DR GO: GO:0005871; C:kinesin complex; IEA.  
 DR GO: GO:0036787; F:hydrolyase activity; IEA.  
 DR GO: GO:0004727; F:prelabeled protein tyrosine phosphatase act. . .; IEA.  
 DR GO: GO:0005198; F:structural molecule activity; IEA.  
 DR GO: GO:0007242; F:intracellular signaling cascade; IEA.  
 DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro: IPR001478; Band\_4.1.  
 DR InterPro: IPR000299; Band\_4.1.  
 DR InterPro: IPR000387; Tyr phosphatase.  
 DR InterPro: IPR000242; Tyr\_Pp.  
 DR Pfam: PF00373; Band\_4.1; I.  
 DR Pfam: PF00395; PDZ\_5.  
 DR Pfam: PF00102; Y\_phosphatase; 1.  
 DR PRINTS: PR00935; BAND41.  
 DR PRINTS: PR00700; PRTPHPTASE.  
 DR SMART: SMO0295; B41.1.  
 DR SMART: SMO0238; PDZ\_5.  
 DR SMART: SMO0194; PTPc\_1.  
 DR PROSITE: PS00660; FERM\_1; FALSE\_NEG.  
 DR PROSITE: PS00661; FERM\_2; FALSE\_NEG.  
 DR PROSITE: PS50057; FERM\_3; 1.  
 DR PROSITE: PS50106; PDZ\_5.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; FALSE\_NEG.  
 DR PROSITE: PS50056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE: PS50055; TYR\_PHOSPHATASE\_PTP; 1.  
 DR Structural protein; Cytoskeleton; Hydrolyase; Repeat; Coiled coil.  
 KM DOMAIN 577 872  
 FT DOMAIN 2203 2460  
 FT ACT\_SITE 2374 2374  
 FT DOMAIN 1084 1940  
 FT REPEAT 1084 1169  
 FT REPEAT 1357 1441  
 FT REPEAT 1490 1577  
 FT REPEAT 1763 1843

FT REPEAT 1858 1940 DHR/GLGF REPEAT 5.  
 FT DOMAIN 371 394 COILED COIL (POTENTIAL).  
 FT DOMAIN 458 493 COILED COIL (POTENTIAL).  
 FT DOMAIN 56 59 POLY-LEU.  
 FT CONFLICT 79 81 STA -> FTG (IN REF. 2).  
 FT CONFLICT 156 168 HIRSNCAPEFSN -> TSGTASRAFYSY (IN REF. 2).  
 FT CONFLICT 233 233 V -> L (IN REF. 2).  
 FT CONFLICT 306 306 N -> I (IN REF. 2).  
 FT CONFLICT 322 322 K -> E (IN REF. 2).  
 FT CONFLICT 381 381 Q -> K (IN REF. 2).  
 FT CONFLICT 822 822 S -> L (IN REF. 2).  
 FT CONFLICT 1233 1233 S -> T (IN REF. 2).  
 FT CONFLICT 1449 1449 R -> Q (IN REF. 2).  
 FT CONFLICT 1474 1488 KHPMSKTALLKTI -> QTPHYKYSFTEDNT (IN REF. 2 AND 3).  
 FT CONFLICT 1621 1621 D -> H (IN REF. 2).  
 FT CONFLICT 1871 1871 P -> S (IN REF. 2 AND 3).  
 FT CONFLICT 1978 1978 N -> I (IN REF. 3).  
 FT CONFLICT 2077 2077 D -> N (IN REF. 2).  
 FT CONFLICT 2232 2232 S -> T (IN REF. 2).  
 FT CONFLICT 2445 2445 Q -> QGLGFQ (IN REF. 2 AND 3).  
 FT CONFLICT 2446 2460 MISSING (IN REF. 2 AND 3).  
 SQ SEQUENCE 2460 AA; 270965 MW; 52F29DE37DE5C807 CRC64;  
 Query Match 26.8%; Score 653; DB 11; Length 2460;  
 Best Local Similarity 35.4%; Pred. No. 2,3e-41;  
 Matches 151; Conservative 67; Mismatches 129; Indels 80; Gaps 8;  
 QY 106 VYEPPELSDTDEVTWVSDRLNRNNSM----- 134  
 DB 2022 IYDDPQAEVLTQSLVVDVEBAQNLNQRATRRACPPPLRTNGAEFEGDTYDGSPL 2091  
 QY 135 -----DSETPGPKTVSPVLSGSSRLSK-----DTETS-----VSE 165  
 DB 2082 PEDVPESVSSGSEKVDLSTLASQEKPIEDATQESNSTTEITDGEDSSODPPLIN 2141  
 QY 166 KSLTQLAQIRPLIFNSARSAMDCINTLQ-----KKEBLDIREFLELQMTLPDDF 218  
 DB 2142 BELAALPVVRVPPSGKYTGQGLQATRTLQGLDQIPSEKELNQLKPLDQCLT---- 2197  
 QY 219 NSGNTLQNDKXRYRLIPVDSRVPLGSKKQYNSYRIYVHHEEYPIANOGPLPT 278  
 DB 2198 --GQTEKRRKKNYKILPDTVRVPLGDEGGINSFIRIPVGTQEPVYIACQGLPTT 2255  
 QY 279 IEDFMQVLENNQNVAMITREIECGVICYSWPISLKEPLFHFVSFTSTFYVTOY 337  
 DB 2256 VGFPMQVMBQNSTVIAMNTQVEGSEKIKQRPSPILGTTMANERLRLALRMQQLNG 2315  
 QY 338 FTVRVQIYKKSIGSKQCYKHLQFTKPDHGPASD---FFIKYRYRKSHITGPLV 394  
 DB 2316 FTVRVVADLDIQGEVRHSHNFTAMPDPHDPSPQDDLLTFISYKHLRRS---GPVIT 2372  
 QY 395 HCSAGVGTGVFCVUVVSAIEKNYSFDIMNIVTMRKORCMQIOKQOYCFEIVAE 454  
 DB 2373 HCSAGIGRSGTILICIVVLGISQDLRFDISLVRCRLQRHGMVGTBOGYVFCYVILX 2432  
 QY 455 VIQNTLLA 461  
 DB 2433 VILTHLOA 2439  
 RESULT 4  
 Q28006 PRELIMINARY; PRT; 2484 AA.  
 ID Q28006;  
 DT 01-NOV-1996 (TEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)  
 DE BA14.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;



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Db      764 HQVMP-----ESESSESSVCYATCHSESSGNPAVYFRKNTLINOENKESROLTOQYTPAMP 815
Qy      366 DHGTPASADFFIKYRYVR--KSHITGPLVHCSAGVGRGVFICVDVFSAIENKYSFD 423
Db      820 DHGVPDDSDLDLPCVCHVRDQAGKEBPIIVHCSAGIGRTGVLLITMETAMCLIECNPVY 879
Qy      424 LNNIVTQMRKORCGMIOFKEOYCFCEYVLEVLQ 457
Db      860 PLDIYRTMRDQPMNITQPSQIRFCCEALIKVYB 913

RESULT 6
ID      Q8NAS3      PRELIMINARY;      PRT;      292 AA.
AC      Q8NAS3;
DT      01-OCT-2002 (TREMBLrel. 22, Created)
DT      01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE      Hypothetical protein (Fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Renal adenocarcinoma;
RA      Strausberg R.;
EMBL    BC033716; AAA33716.1; -.
DR      GO: GO:0005743; C:mitochondrial inner membrane; IEA.
DR      GO: GO:0005488; F:binding; IEA.
DR      GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR      GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR      GO: GO:0006810; P:transport; IEA.
DR      InterPro: IPR001393; Mitoch_carrier.
DR      InterPro: IPR003595; PTPc_motif.
DR      InterPro: IPR000387; TYR_PTP.
DR      Pfam: PF00102; Y_phosphatase; 1.
DR      PRINTS: PR00700; PRTYPHPTASE.
DR      SMART: SM00194; PTPc; 1.
DR      SMART: SM00404; PTPc_motif; 1.
DR      PROSITE: PS00215; MITOCH_CARRIER; 1.
DR      PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR      PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
DR      PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
KW      Hypothetical protein.
FT      NON TER
SQ      SEQUENCE 292 AA; 33121 MW; 54B838BD41D1BD7 CRC64;

Query Match      20.5%; Score 500; DB 4; Length 292;
Best Local Similarity 42.0%; Pred. No. 1e-30;
Matches 102; Conservative 38; Mismatches 85; Indels 18; Gaps 5;

Qy      225 QNRKMRKRDLPDSTRVPLGKXKDYTNASYI-----RIVNHEEYFIATOGPEPE 277
Db      48 QNLDKRRKXDLVPLDYTRKVLQSGNEDYNASVYNNELIPAAVLNKK-----VITATOGPEPE 102
Qy      278 TIEDFWQVAVENNCNVAMITREIECGVIKCYWYPISTKEPFEFH--ESVPLETHVY 335
Db      103 TCAQFWQVAVQDKSLIVMLFTLTERGRKCHQVMP--DEPDVMMHGPFIIQGSDECT 159
Qy      336 QYFVAVVQIVAKSTGKSCQVYKHQFTWMPHGTPASADFFIKYRYRKSHT--TGPELV 394
Db      160 IAYVSRNEMVLTNTQGEHVTYHLOAYAMPDHPGVPDDSDLEFVNYRSLRVDSEPLV 219
Qy      395 HCSAGVGRGVFICVDVFSAIENKYSSEDDINNIYTONMKORCGMIOFKEOYCFCEYVLEB 454
Db      220 HCSAGIGRTGVLLITMETAMCLTERNLPIYPLDIYRKORDDQPMNIVQTSQIKFCCEALIR 279
Qy      455 VLQ 457
Db      280 VYE 282

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RESULT 7
ID      O44328      PRELIMINARY;      PRT;      2051 AA.
AC      O44328;
DT      01-JUN-1998 (TREMBLrel. 06, Created)
DT      01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE      Receptor tyrosine phosphatase.
GN      HMLAR2.
OS      Hirudo medicinalis (Medicinal leech).
OC      Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
OC      Arhynchobdellida; Hirudiniiformes; Hirudiniidae; Hirudo.
NCBI_TaxID=6421;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      MEDLINE=98195364; PubMed=9526016;
RA      Gershon T.R., Baker M.W., Nitabach M., Wu P., Macagno B.R.;
RT      "Two receptor tyrosine phosphatases of theLAR family are expressed in
RT      the developing leech by specific central neurons as well as select
RT      peripheral neurons, muscles, and other cells."
RL      J. Neurosci. 18:2991-3002(1998).
DR      EMBL: AF017083; AAB91460.1; -.
DR      PIR: T30938; T30938.
DR      HSSP: P28827; IRPM.
DR      GO: GO:0016787; F:hydrolase activity; IEA.
DR      GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR      GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR      InterPro: IPR003962; FNIII_subd.
DR      InterPro: IPR003961; FN_III.
DR      InterPro: IPR008957; FN_III-like.
DR      InterPro: IPR007110; IG-like.
DR      InterPro: IPR003598; IG_C2.
DR      InterPro: IPR003387; TYR_phosphatase.
DR      InterPro: IPR000242; TYR_PTP.
DR      Pfam: PF00041; fn3; 8.
DR      Pfam: PF00102; Y_phosphatase; 2.
DR      PRINTS: PR00014; FNTYPEPITII.
DR      PRINTS: PR00700; PRTYPHPTASE.
DR      SMART: SM00060; FN3; 7.
DR      SMART: SM00408; IGc2; 3.
DR      SMART: SM00194; PTPc; 2.
DR      PROSITE: PS50835; IG_LIKE; 3.
DR      PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR      PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR      PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
KW      Hydrolase; Immunoglobulin domain; Repeat.
FT      SEQUENCE 2051 AA; 229604 MW; D60F8A032F659B00 CRC64;

Query Match      20.4%; Score 497; DB 5; Length 2051;
Best Local Similarity 40.3%; Pred. No. 2.3e-29;
Matches 106; Conservative 46; Mismatches 95; Indels 16; Gaps 7;

Qy      205 EPLLEQ-MTLPPDFNSGNTLQNRDKRRDILPYOSTRVPLG-----KKQDIYNASYR 258
Db      1786 EFKLSSGKTSLSFASANLSCMKOKRRLVNVLPYETIRVCLQPIRGVDSQDYINASFID 1845
Qy      259 IVNHEEYFIATOGPEPEIDFWMVLENNNCNVAMITREIECGVIKCYWYPISTKE 318
Db      1846 --GYRRRAVIAINQGLPDEVDPEPALWESNCNIIWLTIKLEMGRKMQVMP--SER 1901
Qy      319 PLEFHPSPV-LETFVNTQYFVAVVQIVAKSTGKSCQVYKHQFTWMPHGTPASADFFI 377
Db      1902 SARVQYFVVDVLAELVNNPQYI-LREKVTYDARQGRTRKQFQLTWMPGQGVSTDDGI 1960
Qy      378 KYRYRYRKS-----LIGPLLVHCSAGVGRGVFICVDVFSAIENKYSSEDDINNIYQMRK 433
Db      1961 DFIGQTHKTRKQFGQGPFAVHCSAGVGRGVFICVDVFSAIENKYSSEDDINNIYQMRK 2020
Qy      434 QRCGMIOFKEOYCFCEYVLEVL 456

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RESULT 10
Q91BA0 PRELIMINARY; PRT; 468 AA.
AC Q91BA0;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE RYTPR2AC protein (Fragment).
GN RYTPR2AC.
OS Potamotrygon motoro (South American freshwater stingray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalae; Hyposquales; Pristiogaster; Batoidae;
OC Myliobatiformes; Myliobatoidei; Potamotrygonidae; Potamotrygon.
NCBI_TaxID=66373;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20219325; PubMed=10754074;
RA Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;
RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:
RT divergence of tissue-specific isoform genes in the early evolution of
RT vertebrates."
RL J. Mol. Evol. 50:302-311(2000).
DR EMBL; AB033586; BAA95193.1; -.
DR HSSP; P18052; 1YFO.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; Tyr_PP.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PRO0700; PRTPHPTASE.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_FTP; 2.
KW Hydrolase.
FT NON TER
SQ SEQUENCE 468 AA; 53976 MW; 76C975D92D437A86 CRC64;

Query Match 20.2%; Score 493.5; DB 13; Length 468;
Best local Similarity 40.2%; Pred. No. 6.1e-30;
Matches 107; Conservative 46; Mismatches 90; Indels 21; Gaps 7;

QY 207 LBLEQMTLPDD-----FNSGNTLQNRDKRRYDIIPYSTRYPLG-----KAKDYINAS 255
DB 200 MELEPKRLANSKXHTSFISANLPCKFKRLVNMVETTRVCIQPIRGVSGSDYINAS 259
QY 256 YRIIVNHEEYFIATOGPLPETIEDFMQVVLNNCNVIMATREIEGVIKCYSTWPIIS 315
DB 260 FID--GRQQKAVIATOGPLAETTEDFMRLMENNSTIIVMLTKLEMGSEKCHQYWP-- 315
QY 316 LKPELEPEHSVE-LETFHTQYFYRVFOIVKSTGKSQCVNHLQFTKMPDHGTASAD 374
DB 316 AESSAYQYVVDPMAEYNNPQYI-LREFKVTARBGQSTRTVQPGFTDMPESGCVKSGE 374
QY 375 FFIKYVRYVRKSH---ITGPLLVHCSAGVGRGVFI CDVVSALIKKYSFDIMNIIVTQ 430
DB 375 GFIDPFGVAKTKRQSGQDDPISVHCSAGVGRGVFTLSTILERRRYEGVVDIPGVNM 434
QY 431 MRKQRCGMTOFKROYOCVEIVLEVL 456
DB 435 LRTQRPAMVGTEDYDTCYQALLEYL 460

RESULT 11
Q90YJ4 PRELIMINARY; PRT; 857 AA.
AC Q90YJ4;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

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DE Receptor protein-tyrosine phosphatase sigma (Fragment).
GN PTPRS OR RPTPSTIGMA.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA van der Sar A., Bellet M., de Pockert J., Overvoorde J., Zivkovic D.,
RA den Hertog J.;
RT "Expression of receptor protein-tyrosine phosphatase alpha, sigma and
RT LAR during development of the zebrafish embryo."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ111886; CAC44759.1; -.
DR ZFIN; ZDB-GENE-020107-3; ptprs.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; FN III-like.
DR InterPro; IPR000242; Tyr_PP.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PRO0700; PRTPHPTASE.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_FTP; 2.
KW Hydrolase.
FT NON TER
SQ SEQUENCE 857 AA; 97709 MW; 604A926B08B81D8 CRC64;

Query Match 20.2%; Score 493.5; DB 13; Length 857;
Best local Similarity 38.1%; Pred. No. 1.4e-29;
Matches 110; Conservative 54; Mismatches 102; Indels 23; Gaps 8;

QY 186 AMRDCINTLQKKEBLDIREF--LELEQMTLPDD-----FNSGNTLQNRDKRRYDIIP 237
DB 566 AARSLSFYIQLQAYEAGHVSQMELEFRLANSKXHTSFISANLPCKFKRLVNMV 625
QY 238 YDSTRVPLG-----KAKDYINASYRIIVNHEEYFIATOGPLPETIEDFMQVVLNNCN 292
DB 626 YETTRVCIQPIRGVSGSDYINASFTD--GYRQQKAVIATOGPLAETTEDFMRLMENNST 683
QY 293 VIAMITREIEGVIKCYSTWPIISLKEPLEPEHSVE-LETFHTQYFYRVFOIVKSTG 351
DB 684 IYVMLTKLEMRERKCHQYWP--AARSARYQYFVVDPMAEYNNPQYI-LREFKVTARBG 740
QY 352 KQCCVNHLOFTKMPDHGTASADFFIKYVRYVRKSH---ITGPLLVHCSAGVGRGVFI 407
DB 741 QSRTRVQFOFTDMPESGCVKSGEFTDIPGVAKTKRQSGQDDPISVHCSAGVGRGVFI 800
QY 408 CDVVSALIKKYSFDIMNIIVTQMRKQRCGMTOFKROYOCVEIVLEVL 456
DB 801 TISTILERRRYEGVVDIPGVNMRTQRPAMVGTEDYDTCYQALLEYL 849

RESULT 12
Q91BA2 PRELIMINARY; PRT; 468 AA.
AC Q91BA2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE RYTPR2AB protein (Fragment).
GN RYTPR2AB.
OS Potamotrygon motoro (South American freshwater stingray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalae; Hyposquales; Pristiogaster; Batoidae;
OC Myliobatiformes; Myliobatoidei; Potamotrygonidae; Potamotrygon.
NCBI_TaxID=66373;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=20219325; PubMed=10754074;  
RA Omo-Koyanagi K., Suga H., Katoh K., Miyata T.;  
RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:  
RT divergence of tissue-specific isoform genes in the early evolution of  
RT vertebrates.";  
RL J. Mol. Evol. 50:302-311(2000).  
DR EMBL; AB033584; BAA95191.1; -.  
DR HSSP; P18052; 1YFO.  
DR GO; GO:0016787; F:Hydrolase activity; IEA.  
DR GO; GO:0004725; F:Protein tyrosine phosphatase activity; IEA.  
DR GO; GO:0004720; P:Protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR000387; Tyr\_phosphatase.  
DR InterPro; IPR000242; Tyr\_PP.  
DR Pfam; PF00102; Y\_phosphatase; 2.  
DR PRINTS; PR00700; PRTPHPHPTASE.  
DR SMART; SM00194; PTPC; 2.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 2.  
DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 2.  
DR Hydrolase.  
KW NON TER  
SQ SEQUENCE 468 AA; 53885 MW; 8B1CAB0E8E9692E4 CRC64;  
Query Match 20.2%; Score 491.5; DB 13; Length 468;  
Best Local Similarity 40.6%; Pred. No. 8.7e-30;  
Matches 108; Conservative 46; Mismatches 91; Indels 21; Gaps 7;  
QY 207 LELERQMLPPD-----FNSGNTLQNRDKNRDILPSTYPLG-----KQKDYINAS 255  
DB 200 MELEFKLALTKAHTSRFTISANLPCNFKRNLVIMVESTRVCLQIRGVEGSDYINAS 259  
QY 256 YIRVNHSEEFYKACGGPLPTEDEDMQWLENNCNVIMTRIECGVTKCYSPIS 315  
DB 260 FID--GRQCAVATATGCPLETTEDFWRLMEHNSITVNLVTLGRMEKCHQTF-- 315  
QY 316 LKEPLREHSEVF--LETFHYQVPTVAVFOIVKSKTSQCVKHLQTKWPDHGTASAD 374  
DB 316 AERBARQYFYVDMAAYNMPQY--LNEFYTDARQDSRTVRQFQTDWPEQGVKSGE 374  
QY 375 FFIVYVYVYKSH---ITGPLVHCSAGVGTGVCVDVVSALIKYNSFDIMNIVYQ 430  
DB 375 GFIFDIOGVNHTKQDFQDGPISVHCSAGVGTGVTITLSTVLERMEYEGVVDLPQTKM 434  
QY 431 MRKRCGMITQKEQYQFCYEIVLEVL 456  
DB 435 LRTORPAMVQTBQYQFCYRALHYL 460

RESULT 13  
Q90947 PRELIMINARY; PRT; 832 AA.  
AC Q90947;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Phosphotyrosyl phosphatase.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=94122757; PubMed=8293038;  
RA Darker D.L., Branton P.E.;  
RA "Isolation of chicken phosphotyrosyl phosphatase cDNA sequences and  
RA identification of a brain-specific species related to human PTPzeta.";  
RL Cell. Mol. Biol. Res. 39:209-219(1993).  
DR EMBL; L27625; AAA49015.1; -.  
DR HSSP; P18052; 1YFO.  
DR GO; GO:0016787; F:Hydrolase activity; IEA.

DR GO; GO:0004725; F:Protein tyrosine phosphatase activity; IEA.  
DR GO; GO:0004720; F:Protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR000387; Tyr\_phosphatase.  
DR InterPro; IPR000242; Tyr\_PP.  
DR Pfam; PF00102; Y\_phosphatase; 2.  
DR PRINTS; PR00700; PRTPHPHPTASE.  
DR SMART; SM00194; PTPC; 2.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 2.  
DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 2.  
DR Hydrolase.  
KW  
SQ SEQUENCE 832 AA; 93298 MW; 4A61F365BD794F3 CRC64;  
Query Match 20.2%; Score 491.5; DB 13; Length 832;  
Best Local Similarity 27.6%; Pred. No. 1.9e-29;  
Matches 141; Conservative 89; Mismatches 177; Indels 109; Gaps 16;  
QY 23 GNILNLSLSPSSSQMTPTKPVQNKILMK---YREHDLIWLFLIKTIMVNFILMKK 79  
DB 34 GNLWFRNATELTSQ---PVGTWDSHLSQTSYTDYVEGLKP---ATVPYS-----GS 80  
QY 80 LIFGNKNSENVKPSHHLSFSDKELVYPEPELSTQDETVMVDSRLNKNNSDSETA 139  
DB 81 PVVSQDTSDVDLELPHYSTFAFSALPRLHSLSSSGE-----YGSASASE 127  
QY 140 GPKTVPYLSGSSRLSKDTSTVSSEKELYQLAQLRPLIFNSASA-----NR 188  
DB 128 VLSQITQPIYNASNSHSHRIGLASESEKKYVPLVVSALFICVLIVGLIYR 187  
QY 189 DCLNLTQ-----KKEHLDI-----IREPLE 208  
DB 188 KCFQTAHFLIEDNTSPVISAAPAFVPSVDVGAIPKHPKRVADLASNGSFSEFE 247  
QY 209 LEQMT--LEDDNSGNTLQNRDKNRDILPSTYPLG-----GKKDYINASYIRI 259  
DB 248 IGSCTVDLITSSSNHPKNNKRYINVAIDHRTVLAQLAKDQKLDVYNAYVQ 307  
QY 260 VNHSEEFYIATQGPLPTEDEDMQWLENNCNVIMTRIECGVTKCYSPISLKEP 319  
DB 308 VNNPKA--YIAAGPLKSTAEDEFWRIWEHNEVAVIMTNLEKRRKDDQVPAQSGE- 364  
QY 320 LEPEHSEVFLETFHYQVPTVAVFOIVKSKTSQCVKHLQTKWPDHGTASAD 374  
DB 365 -EYGNLVTKSHVAVIYVNRFTLRNTKIKKSGKSSGSRVYQYHTQWPDGVP- 422  
QY 372 SADPFKYRVYVYKSH---HTGPLVHCSAGVGTGVCVDVVSALIKYNSFDIMN 426  
DB 423 --EYTLPVLTFRKSHAKRHAHVGIIVHCSAGVGTGVTYVLDLYLQIQIHGVTNIRG 480  
QY 427 IYTVKRCGMITQKEQYQFCYEIVLEVL 456  
DB 481 FLKHRTQRYNVQTBQYQFCYRALHYL 510

RESULT 14  
Q90981 PRELIMINARY; PRT; 1502 AA.  
AC Q90981;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Pepsigma-(brain) precursor.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Endo N., Rutledge S.J., Opas E.B., Vogel R., Rodan G.A., Schmidt A.;  
RA "Human protein tyrosine phosphatase-sigma: Alternative splicing and  
RA inhibition by diisophosphates.";  
RL J. Bone Miner. Res. 0:0-0(1995).

DR EMBL: U41725; AAD09360.1; -.  
 DR HSRP: P18052; IYPO.  
 DR GO: GO:0016787; F:Hydrolase activity; IEA.  
 DR GO: GO:0006475; P:Protein tyrosine phosphatase activity; IEA.  
 DR GO: GO:0006470; P:Protein amino acid dephosphorylation; IEA.  
 DR InterPro: IPR003962; FNIII subd.  
 DR InterPro: IPR003961; FN III.  
 DR InterPro: IPR008957; FN\_III-like.  
 DR InterPro: IPR007110; IG\_1-like.  
 DR InterPro: IPR003598; IG\_c2.  
 DR InterPro: IPR000387; TYR\_phosphatase.  
 DR InterPro: IPR000242; TYR\_pp.  
 DR Pfam: PF00047; FN3; 4.  
 DR Pfam: PF00047; IG; 3.  
 DR Pfam: PF00102; Y\_phosphatase; 2.  
 DR PRINTS: PR00014; FNTYPPHIT.  
 DR PRINTS: PR00700; PRTYPPHITASB.  
 DR SMART: SM00060; FN3; 4.  
 DR SMART: SM00408; IGc2; 2.  
 DR SMART: SM00194; PTPc; 2.  
 DR PROSITE: PS00835; IG\_LIKE; 3.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE: PS00056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE: PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 DR HydroLase; Immunoglobulin domain; Signal.  
 FT SIGNAL 1 28  
 SQ SEQUENCE 1502 AA; 16878 MW; AD6705AFEB0F3CFD CRC64;

Query March 20.1%; Score 490.5; DB 4; Length 1502;  
 Best Local Similarity 40.2%; Pred. No. 4.9e-28;  
 Matches 107; Conservative 47; Mismatches 91; Indels 21; Gaps 7;  
 QY 207 LELEQMTLPDD-----FNSGNTLQNRDKKRYRDIIPYDSTRVPLG-----KKNQDYINAS 255  
 DB 1234 MELEFKRLASKKHTSRFISANLPCNKKFKRLVNIWYESTRYCLQPIRGVBSGDIYNAS 1293  
 QY 256 YIRIVNHEEYFIATOGPLPETIEDPWQVLENNCNVIMITREIBGVIKCYSTWPIS 315  
 DB 1294 FID--GYRQOKAYIATOGPLAETTEDFWRLMENNSTIVMLTKLRMGREKCHQYWP-- 1349  
 QY 316 LKEPLEFHFSPV-LETFHYQVFTVRFVFOIVKSKTSKSCVHQLQFTKPDHGTASAD 374  
 DB 1350 AERSARQYFVVDPMALYNNPQYI-LREFKYTDARQSRVTRQFQFTDMPGQVPSGGE 1408  
 QY 375 PFIKYRVYRKSH---ITGPLLHCSAGVGRGVFCVDVFSALIKNYSFDIMNIYVQ 430  
 DB 1409 GFIDFICGVHKTKEQFGQDGPISVHCSAGVGRGVFTLISILVRMYRGVVDIFQTVKM 1468  
 QY 431 MKRQRCGMQTKQVQFCYEIVLEVL 456  
 DB 1469 LRTQRPAMVQTEBDQYQCYRAALEYL 1494

RESULT 15  
 QSR169 PRELIMINARY; PRT; 749 AA.  
 ID QSR169  
 AC QSR169;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NX NCBI\_TaxID=10090;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Strausberg R.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC025145; AAH25145.1; -.  
 DR PIR: S40282; S40282.  
 DR GO: GO:0016787; F:Hydrolase activity; IEA.

DR GO: GO:0006475; P:Protein tyrosine phosphatase activity; IEA.  
 DR GO: GO:0006470; P:Protein amino acid dephosphorylation; IEA.  
 DR InterPro: IPR000387; TYR\_phosphatase.  
 DR InterPro: IPR000242; TYR\_pp.  
 DR Pfam: PF00102; Y\_phosphatase; 2.  
 DR PRINTS: PR00700; PRTYPPHITASB.  
 DR SMART: SM00194; PTPc; 2.  
 DR PROSITE: PS00835; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE: PS00056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE: PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 DR Hypothetical protein; Hydrolase.  
 SQ SEQUENCE 749 AA; 86082 MW; 421FC6B9B50C959E CRC64;

Query March 20.1%; Score 489.5; DB 11; Length 749;  
 Best Local Similarity 40.2%; Pred. No. 2.3e-29;  
 Matches 107; Conservative 46; Mismatches 92; Indels 21; Gaps 7;  
 QY 207 LELEQMTLPDD-----FNSGNTLQNRDKKRYRDIIPYDSTRVPLG-----KKNQDYINAS 255  
 DB 481 MELEFKRLASKKHTSRFISANLPCNKKFKRLVNIWYESTRYCLQPIRGVBSGDIYNAS 540  
 QY 256 YIRIVNHEEYFIATOGPLPETIEDPWQVLENNCNVIMITREIBGVIKCYSTWPIS 315  
 DB 541 FID--GYRQOKAYIATOGPLAETTEDFWRLMENNSTIVMLTKLRMGREKCHQYWP-- 596  
 QY 316 LKEPLEFHFSPV-LETFHYQVFTVRFVFOIVKSKTSKSCVHQLQFTKPDHGTASAD 374  
 DB 597 AERSARQYFVVDPMALYNNPQYI-LREFKYTDARQSRVTRQFQFTDMPGQVPSGGE 655  
 QY 375 PFIKYRVYRKSH---ITGPLLHCSAGVGRGVFCVDVFSALIKNYSFDIMNIYVQ 430  
 DB 656 GFIDFICGVHKTKEQFGQDGPISVHCSAGVGRGVFTLISILVRMYRGVVDIFQTVKM 715  
 QY 431 MKRQRCGMQTKQVQFCYEIVLEVL 456  
 DB 716 LRTQRPAMVQTEBDQYQCYRAALEYL 741

Search completed: June 18, 2004, 19:40:03  
 Job time : 49 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: June 18, 2004, 19:40:39 ; Search time 59 Seconds  
(without alignments)  
2217.280 Million cell updates/sec

Title: US-09-095-478a-6

Perfect score: 463

Sequence: 1 MSPPRYKRGKTRNDDEEG.....QYCFYIVLAVLQNLALY 463

Scoring table: OLIGO

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_29Jan04.\*

1: geneseqp1980s.\*  
2: geneseqp1990s.\*  
3: geneseqp2000s.\*  
4: geneseqp2001s.\*  
5: geneseqp2002s.\*  
6: geneseqp2003s.\*  
7: geneseqp2003ds.\*  
8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	463	100.0	463	2	AAW89250 Mouse PTP
2	383	82.7	426	2	AAW89249 Mouse PTP
3	362	78.2	405	2	AAW89251 Mouse PTP
4	29	6.3	29	2	AAW89264 Human PTP
5	29	6.3	29	2	AAW89263 Human PTP
6	29	6.3	29	2	AAW89265 Human PTP
7	23	5.0	122	2	AAW89252 Rat PTP10
8	19	4.1	261	5	AAW89254 Human kin
9	19	4.1	398	5	ABG30845 Human tyr
10	19	4.1	398	7	ADD89795 Human Dkr
11	19	4.1	409	7	ADD09123 Novel pro
12	19	4.1	412	6	AAW89296 Human kin
13	19	4.1	420	5	AAW89265 Human PTP
14	19	4.1	508	7	ADD08106 Novel pro
15	19	4.1	561	4	ABG06042 Novel hum
16	15	3.2	272	2	AAW67441 N-term
17	15	3.2	272	2	AAW67441 N-term
18	15	3.2	1105	4	AAW34161 Human PTP
19	15	3.2	1174	2	AAW5567 Human pro
20	15	3.2	1174	2	AAW67438 Human pro
21	15	3.2	1174	2	AAW34158 Human pro
22	15	3.2	1175	7	ADD45494 Human pro
23	15	3.2	1175	7	ADD45494 Human pro
24	15	3.2	1175	7	ADD45494 Human pro
25	14	3.0	176	2	AAW61033 Rat Prote
					AAW60876 Product o

## ALIGNMENTS

RESULT 1	AAW89250 standard: protein; 463 AA.
ID	AAW89250
AC	AAW89250;
DT	10-MAR-1999 (first entry)
XX	Mouse PTP05 isoform #1.
DE	PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzheimer's disease; Parkinson's disease; Huntington's disease.
KW	Mus sp.
OS	Mus sp.
PN	MO9849317-A2.
XX	05-NOV-1998.
PD	05-NOV-1998.
XX	27-APR-1998; 98WO-US008439.
PF	28-APR-1997; 97US-0044428P.
XX	20-MAY-1997; 97US-0047222P.
PR	11-JUN-1997; 97US-0049477P.
XX	11-JUN-1997; 97US-0049756P.
PR	18-JUN-1997; 97US-0049914P.
XX	23-OCT-1997; 97US-0063595P.
PA	(SUGB-) SUGEN INC.
XX	Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markey D; Courtneidge SA, App H, Hui TH; WPI: 1999-009434/01.
DR	N-PSDB: AAW81745.
XX	New nucleic acid encoding specific protein tyrosine phosphatases - useful for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease.
PT	Claim 2; Page 157-158; 1999p: English.
XX	The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, ALP and ALK-7 proteins. The present sequence represents mouse PTP05. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify



RESULT 3  
AAW89251  
ID AAW89251 standard; protein; 405 AA.  
XX  
AC AAW89251;  
XX  
DT 10-MAR-1999 (first entry)  
XX  
DE Mouse PTP05 isoform #2.  
XX  
KM PTP04; PTP05; SAD; ALP; ALK-7; protein tyrosine phosphatase;  
KM type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;  
KM neurodegenerative disease; neuronal survival; Alzheimer's disease;  
KM Parkinson's disease; Huntington's disease.  
XX  
OS Mus sp.  
XX  
EN WO9849317-A2.  
XX  
PD 05-NOV-1998.  
XX  
PE 27-APR-1998; 98WO-US008439.  
XX  
PR 28-APR-1997; 97US-0044428P.  
PR 20-MAY-1997; 97US-0047222P.  
PR 11-JUN-1997; 97US-0049477P.  
PR 11-JUN-1997; 97US-0049756P.  
PR 18-JUN-1997; 97US-0049914P.  
PR 23-OCT-1997; 97US-0063595P.  
XX  
PA (SUGEN-) SUGEN INC.  
XX  
PI Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;  
PI Courtenidge SA, App H, Hui TH;  
XX  
XX WPI; 1999-009434/01.  
XX  
DR N-PSDB; AAV81746.  
XX  
PT New nucleic acid encoding specific protein tyrosine phosphatases - useful  
PT for identifying specific modulators for treatment and prevention of  
PT cancer and neurodegenerative disease.  
XX  
PS Claim 2; Page 158-160; 193pp; English.  
XX  
CC The present invention describes isolated, enriched or purified nucleic  
CC acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The  
CC present sequence represents mouse PTP05. The above proteins, other than  
CC ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify  
CC substances that modulate their activity (i.e. agonists and antagonists,  
CC including NBP) in vivo or in vitro. These substances are used to treat or  
CC prevent diseases associated with abnormal signal transduction pathways  
CC that involve the proteins, particularly cancer (e.g. leukaemia and  
CC lymphoma), while modulators of ALK-7 (which is a type I receptor  
CC serine/threonine kinase) are used to promote neuronal survival,  
CC particularly for treating Alzheimer's, Parkinson's or Huntington's  
CC diseases. Nucleic acid fragments of the polynucleotides encoding the  
CC proteins can be used as probes to identify and clone related sequences;  
CC to detect protein-encoded RNA; to generate transgenic animals and in gene  
CC therapy (optionally after mutation). Ab are used to determine the  
CC proteins  
XX  
SQ Sequence 405 AA;

Query Match 78.2%; Score 362; DB 2; Length 405;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 IFGNKNSSEVKKSHHSFSDKYLEVPEPLESDTDTETWDVDSIRNRKNSMDESTKG 140  
DB 44 IFGNKNSSEVKKSHHSFSDKYLEVPEPLESDTDTETWDVDSIRNRKNSMDESTKG 103

QY 141 PSKTVSPVLSGSSRLSDMTETSYSEKELTOLAQIRPLIFNSSARSARMDCLNTLQKEEL 200  
DB 104 PSKTVSPVLSGSSRLSDMTETSYSEKELTOLAQIRPLIFNSSARSARMDCLNTLQKEEL 163  
QY 201 DIIRFLELEQMTLPDDFNSGNTLQNRDKNRVBDILPYDSTRVPLGKNKYINASYIRIV 260  
DB 164 DIIRFLELEQMTLPDDFNSGNTLQNRDKNRVBDILPYDSTRVPLGKNKYINASYIRIV 223  
QY 261 NHEBEVYIATQGPLPETIEDFWQMTLENKCNITAMITRIEGGVIKCYSYWPISLKEPL 320  
DB 224 NHEBEVYIATQGPLPETIEDFWQMTLENKCNITAMITRIEGGVIKCYSYWPISLKEPL 283  
QY 321 EPEHFSVLETFVATQYFVRFQIVKSGKSCVCHLOFTKMPDHPGTSADFFIKYV 380  
DB 284 EPEHFSVLETFVATQYFVRFQIVKSGKSCVCHLOFTKMPDHPGTSADFFIKYV 343  
QY 381 RYVRKSHITGPIPLVHGSAGVGRGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCMIQ 440  
DB 344 RYVRKSHITGPIPLVHGSAGVGRGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCMIQ 403  
QY 441 TK 442  
DB 404 TK 405

RESULT 4  
AAW89264  
ID AAW89264 standard; peptide; 29 AA.  
XX  
AC AAW89264;  
XX  
DT 10-MAR-1999 (first entry)  
XX  
DE Human PTP05 peptide 431A.  
XX  
KM PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;  
KM type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;  
KM neurodegenerative disease; neuronal survival; Alzheimer's disease;  
KM Parkinson's disease; Huntington's disease.  
XX  
OS Homo sapiens.  
XX  
EN WO9849317-A2.  
XX  
PD 05-NOV-1998.  
XX  
PE 27-APR-1998; 98WO-US008439.  
XX  
PR 28-APR-1997; 97US-0044428P.  
PR 20-MAY-1997; 97US-0047222P.  
PR 11-JUN-1997; 97US-0049477P.  
PR 11-JUN-1997; 97US-0049756P.  
PR 18-JUN-1997; 97US-0049914P.  
PR 23-OCT-1997; 97US-0063595P.  
XX  
PA (SUGEN-) SUGEN INC.  
XX  
PI Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;  
PI Courtenidge SA, App H, Hui TH;  
XX  
XX WPI; 1999-009434/01.  
XX  
PT New nucleic acid encoding specific protein tyrosine phosphatases - useful  
PT for identifying specific modulators for treatment and prevention of  
PT cancer and neurodegenerative disease.  
XX  
PS Example 14; Page 108; 193pp; English.  
XX  
CC The present invention describes isolated, enriched or purified nucleic  
CC acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The  
CC above proteins, other than ALK-7, are protein tyrosine phosphatases  
CC (PTPs) and are used to identify substances that modulate their activity  
CC (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These

CC substances are used to treat or prevent diseases associated with abnormal  
 CC signal transduction pathways that involve the proteins, particularly  
 CC cancer (e.g. leukemia and lymphoma), while modulators of ALK-7 (which is  
 CC a type I receptor serine/threonine kinase) are used to promote neuronal  
 CC survival, particularly for treating Alzheimer's, Parkinson's or  
 CC Huntington's diseases. Nucleic acid fragments of the polynucleotides  
 CC encoding the proteins can be used as probes to identify and clone related  
 CC sequences; to detect protein-encoded RNA; to generate transgenic animals  
 CC and in gene therapy (optionally after mutation). Ab are used to determine  
 CC the proteins. The present sequence represents a human PTP05 peptide from  
 CC the present invention

XX Sequence 29 AA;

XX SQ  
 XX Query Match 6.3%; Score 29; DB 2; Length 29;  
 XX Best Local Similarity 100.0%; Pred. NO. 1.4e-21;  
 XX Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 146 SPVLSSSRSLSKDTETSVSEKELTQLAQI 174  
 DB 1 SPVLSSSRSLSKDTETSVSEKELTQLAQI 29

RESULT 5  
 ID AAW89263 standard; peptide; 29 AA.  
 XX AAW89263;

XX 10-MAR-1999 (first entry)

XX Human PTP05 peptide 433A.

XX PTP04; PTP05; SAD; ALP; ALK-7; protein tyrosine phosphatase;  
 XX type I receptor serine/threonine kinase; cancer; leukemia; lymphoma;  
 XX neurodegenerative disease; neuronal survival; Alzheimer's disease;  
 XX Parkinson's disease; Huntington's disease.

XX Homo sapiens.

XX WO9849317-A2.

XX 05-NOV-1998.

XX 27-APR-1998; 98WO-US008439.

XX 28-APR-1997; 97US-0044428P.

XX 20-MAY-1997; 97US-0047222P.

XX 11-JUN-1997; 97US-0049477P.

XX 18-JUN-1997; 97US-0049756P.

XX 23-OCT-1997; 97US-0063595P.

XX (SUGEN-) SUGEN INC.

XX Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;  
 XX Courtenidge SA, App H, Hui TH;

XX WPI; 1999-009434/01.

XX New nucleic acid encoding specific protein tyrosine phosphatases - useful  
 XX for identifying specific modulators for treatment and prevention of  
 XX cancer and neurodegenerative disease.

XX Example 14; Page 108; 193pp; English.

XX The present invention describes isolated, enriched or purified nucleic  
 XX acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The  
 XX above proteins, other than ALK-7, are protein tyrosine phosphatases  
 XX (PTPs) and are used to identify substances that modulate their activity  
 XX (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These  
 XX substances are used to treat or prevent diseases associated with abnormal  
 XX signal transduction pathways that involve the proteins, particularly

CC cancer (e.g. leukemia and lymphoma), while modulators of ALK-7 (which is  
 CC a type I receptor serine/threonine kinase) are used to promote neuronal  
 CC survival, particularly for treating Alzheimer's, Parkinson's or  
 CC Huntington's diseases. Nucleic acid fragments of the polynucleotides  
 CC encoding the proteins can be used as probes to identify and clone related  
 CC sequences; to detect protein-encoded RNA; to generate transgenic animals  
 CC and in gene therapy (optionally after mutation). Ab are used to determine  
 CC the proteins. The present sequence represents a human PTP05 peptide from  
 CC the present invention

XX SQ  
 XX Sequence 29 AA;

XX Query Match 6.3%; Score 29; DB 2; Length 29;  
 XX Best Local Similarity 100.0%; Pred. NO. 1.4e-21;  
 XX Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSSPRRYRGKTRGNDREBGSNGNLNLRN 29  
 DB 1 MSSPRRYRGKTRGNDREBGSNGNLNLRN 29

RESULT 6  
 ID AAW89265 standard; peptide; 29 AA.  
 XX AAW89265;

XX 10-MAR-1999 (first entry)

XX Human PTP05 peptide 432A.

XX PTP04; PTP05; SAD; ALP; ALK-7; protein tyrosine phosphatase;  
 XX type I receptor serine/threonine kinase; cancer; leukemia; lymphoma;  
 XX neurodegenerative disease; neuronal survival; Alzheimer's disease;  
 XX Parkinson's disease; Huntington's disease.

XX Homo sapiens.

XX WO9849317-A2.

XX 05-NOV-1998.

XX 27-APR-1998; 98WO-US008439.

XX 28-APR-1997; 97US-0044428P.

XX 20-MAY-1997; 97US-0047222P.

XX 11-JUN-1997; 97US-0049477P.

XX 18-JUN-1997; 97US-0049756P.

XX 23-OCT-1997; 97US-0063595P.

XX (SUGEN-) SUGEN INC.

XX Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;  
 XX Courtenidge SA, App H, Hui TH;

XX WPI; 1999-009434/01.

XX New nucleic acid encoding specific protein tyrosine phosphatases - useful  
 XX for identifying specific modulators for treatment and prevention of  
 XX cancer and neurodegenerative disease.

XX Example 14; Page 108; 193pp; English.

XX The present invention describes isolated, enriched or purified nucleic  
 XX acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The  
 XX above proteins, other than ALK-7, are protein tyrosine phosphatases  
 XX (PTPs) and are used to identify substances that modulate their activity  
 XX (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These  
 XX substances are used to treat or prevent diseases associated with abnormal  
 XX signal transduction pathways that involve the proteins, particularly  
 XX cancer (e.g. leukemia and lymphoma), while modulators of ALK-7 (which is  
 XX a type I receptor serine/threonine kinase) are used to promote neuronal





CC diagnosing, treating or preventing disorders associated with aberrant  
CC expression of KRP, particularly cell proliferative disorders (e.g.  
CC arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal  
CC nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary  
CC thrombocytopaenia or cancer), developmental disorders (eg. renal tubular  
CC acidosis, anaemia or mental retardation), neurological disorders (e.g.  
CC Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune/  
CC inflammatory disorders (e.g. AIDS, acquired immune deficiency syndrome,  
CC allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's  
CC disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome,  
CC gout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome,  
CC multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's  
CC syndrome, Rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,  
CC bacterial, fungal, parasitic, protozoan or helminthic infections. The KRP  
CC is useful in assessing the effects of exogenous compounds on the  
CC expression of nucleic acids and kinases and phosphatases. The KRP gene is  
CC useful in gene therapy and for creating transgenic animals to model human  
CC disease. The present sequence is human KRP protein

CC Sequence 261 AA;

Query Match 4.1%; Score 19; DB 6; Length 261;  
Best Local Similarity 100.0%; Pred. No. 1.8e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 KRRYRDILPYDSTRVPLGK 247  
DB 27 KRRYRDILPYDSTRVPLGK 45

RESULT 9  
ID ABG30845 standard; protein, 398 AA.

AC ABG30845;

XX 21-OCT-2002 (first entry)

XX Human tyrosine phosphatase protein #1.

XX Human; tyrosine phosphatase; obesity; diabetes; Parkinson's disease;  
XX central nervous system disorder; CNS; cardiovascular disorder; stroke;  
XX chronic obstructive pulmonary disease; cancer; multiple sclerosis;  
XX Alzheimer's disease; Huntington's disease; congestive heart failure;  
XX myocardial infarction; chromosome 10.

XX Homo sapiens.

OS WO200242435-A2.

XX 30-MAY-2002.

XX 27-NOV-2001; 2001WO-EP013794.

XX 27-NOV-2000; 2000US-0252912P.

XX (FARB ) BAYER AG.

XX Zhu Z;

XX WPI; 2002-575236/61.

XX N-PSDB; ABR89178.

XX New human tyrosine phosphatase polypeptide, the regulation of which is  
XX useful for treating obesity, diabetes, cardiovascular or central nervous  
XX system disorder, chronic obstructive pulmonary disease and cancer.

XX Claim 25; Fig 2; 145P; English.

XX The present invention relates to a new human tyrosine phosphatase  
XX polypeptide. The invention is useful for the preparation of a medicament  
XX for modulating the activity of human tyrosine phosphatase in a disease  
XX such as obesity, diabetes, a central nervous system (CNS) disorder.

CC chronic obstructive pulmonary disease, cardiovascular disorder or cancer.  
CC The invention is useful for treating a human tyrosine phosphatase  
CC dysfunction related disease, preferably the above mentioned diseases. The  
CC invention is useful for treating the above mentioned disorders, where the  
CC CNS disorder is selected from Parkinson's disease, multiple sclerosis,  
CC stroke, Alzheimer's disease, and Huntington's disease, and the  
CC cardiovascular disorder is selected from congestive heart failure and  
CC myocardial infarction. The molecules of the invention are useful in  
CC diagnostic assays for detecting diseases and abnormalities or  
CC susceptibility to disease and abnormalities related to the presence of  
CC mutations in the polynucleotide coding the polypeptide of the invention.  
CC The present amino acid sequence represents the human tyrosine phosphatase  
CC protein #1 of the invention. This sequence is encoded by the human  
CC tyrosine phosphatase gene located on chromosome 10

CC Sequence 398 AA;

Query Match 4.1%; Score 19; DB 5; Length 398;  
Best Local Similarity 100.0%; Pred. No. 2.7e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 KRRYRDILPYDSTRVPLGK 247  
DB 164 KRRYRDILPYDSTRVPLGK 182

RESULT 10  
ID ADB89795 standard; protein, 398 AA.

AC ADB89795;

XX 29-JAN-2004 (first entry)

XX Human DKFZP56K0524 protein SEQ ID NO:10.

XX cancer associated phosphatase; enzyme; human; cancer; tumour; cytostatic;  
XX immunosuppressive; antidiabetic; neuroprotective; antithematic;  
XX articular; antiproliferative; antiarteriosclerotic; antiinflammatory;  
XX vulnary; gynaecological; antiangiogenic; hyperproliferative disease;  
XX autoimmune disease; diabetes mellitus; multiple sclerosis;  
XX rheumatoid arthritis; psoriasis; atherosclerosis; inflammation; scarring;  
XX endometriosis; angiogenesis.

XX Homo sapiens.

OS WO2003083102-A2.

XX 09-OCT-2003.

XX 19-MAR-2003; 2003WO-CA00093.

XX 28-MAR-2002; 2002US-0368859P.

XX (KINE-) KINETEK PHARM INC.

XX Delaney AD;

XX WPI; 2003-902934/82.

XX N-PSDB; ADB89794.

XX New nucleic acids encoding cancer associated phosphatases, useful as  
XX targets for screening pharmaceutical agents that inhibit the growth of  
XX tumor cells, or for diagnosing and treating cancer, inflammation or  
XX autoimmune disease.

XX Claim 1; SEQ ID NO 10; 63P; English.

XX The present invention describes an isolated cancer associated phosphatase  
XX nucleic acid. Also described: (1) a method of screening for biologically  
XX active agents that modulate a cancer associated phosphatase function; (2)  
XX a method for the diagnosis of cancer; (3) a method for inhibiting the  
XX growth of a cancer cell; (4) methods of screening for targets of a cancer

CC associated phosphatase, where the targets are associated with signal  
 CC transduction in cancer cells; (5) a compound (C) for the treatment of a  
 CC tumour; (6) a composition for the treatment of a tumour comprising a  
 CC pharmaceutical carrier and (C); (7) methods for treating a tumour; and  
 CC (8) a method for visualising a tumour in a patient. A cancer associated  
 CC phosphatase of the present invention has cytostatic, immunosuppressive,  
 CC antidiabetic, neuroprotective, antineoplastic, antiarthritic,  
 CC antiproliferative, antiarteriosclerotic, antiinflammatory, vulnary,  
 CC gynaecological and antiangiogenic activities. The cancer associated  
 CC phosphatases and nucleic acids encoding the proteins are useful for  
 CC visualising tumours in patients or diagnosing and treating cancer, e.g.  
 CC pancreas, lung, ovarian, liver or colon cancer. The polypeptides and  
 CC nucleic acids may also be used for treating hyperproliferative diseases,  
 CC such as autoimmune disease, diabetes mellitus, multiple sclerosis,  
 CC rheumatoid arthritis, psoriasis, atherosclerosis, inflammation, scarring,  
 CC endometriosis or angiogenesis, determining the effectiveness of drugs,  
 CC determining patient prognosis, or as targets for screening pharmaceutical  
 CC agents that inhibit the growth or metastasis of tumour cells. The present  
 CC sequence represents the human cancer associated phosphatase  
 CC DKFZP566K0524, which is used in the exemplification of the present  
 CC invention.

CC Sequence 398 AA;

Query Match 4.1%; Score 19; DB 7; Length 398;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 229 KNRVRLDLPYDSTRVPLGK 247  
 DB 164 KNRVRLDLPYDSTRVPLGK 182

RESULT 11

ID ADE09123 standard; protein; 409 AA.

XX ADE09123;

DT 29-JAN-2004 (first entry)

XX Novel protein-related contig polypeptide sequence #189.

XX novel gene; novel protein; tissue marker; molecular weight marker;

XX chromosomal marker; genetic disorder; contig.

XX Unidentified.

XX WO2003054152-A2.

XX 03-JUN-2003.

XX 10-DEC-2002; 2002WO-US039555.

XX 10-DEC-2001; 2001US-0339739P.

XX 11-DEC-2001; 2001US-0339453P.

XX 14-MAR-2002; 2002US-0365091P.

XX 14-MAR-2002; 2002US-0365384P.

XX 12-APR-2002; 2002US-0372381P.

XX 12-APR-2002; 2002US-0372615P.

XX 22-APR-2002; 2002US-00128558.

XX 24-APR-2002; 2002US-0376045P.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;  
 PT Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Dirmannac RT, Wang Z;  
 PT Ma Y, Wang D, Chen R, Xu C, Boyle BJ;  
 DR WPI; 2003-569235/53.  
 XX New polynucleotides, useful for expressing recombinant proteins for  
 PT analysis, characterization or therapeutic use, or as markers for tissues

PT in which the corresponding protein is preferentially expressed.  
 XX Disclosure; SEQ ID NO 2667; 1177pp; English.

XX The invention comprises the amino acid and coding sequences of novel  
 CC proteins. The DNA and protein sequences of the invention are useful as:  
 CC markers for tissues in which the corresponding protein is preferentially  
 CC expressed; as molecular weight markers on gels; as chromosome markers or  
 CC tags; to identify chromosomes or to map related gene positions; and to  
 CC compare with endogenous DNA sequences in patients to identify potential  
 CC genetic disorders. The present amino acid sequence was used in the  
 CC exemplification of the invention.

XX Sequence 409 AA;

Query Match 4.1%; Score 19; DB 7; Length 409;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 229 KNRVRLDLPYDSTRVPLGK 247  
 DB 175 KNRVRLDLPYDSTRVPLGK 193

RESULT 12

ID AAE37996 standard; protein; 412 AA.

XX AAE37996;

DT 06-NOV-2003 (first entry)

XX Human kinase and phosphatase (KCP-41) protein.

XX Human; kinase; phosphatase; KCP; cell proliferative disorder; hepatitis;  
 XX atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer;  
 XX psoriasis; chromobocyclopaenia; developmental disorder; Reiter's syndrome;  
 XX renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease;  
 XX neurological disorder; Parkinson's disease; epilepsy; glomerulonephritis;  
 XX autoimmune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome;  
 XX acquired immune deficiency syndrome; immunosuppressive; Crohn's disease;  
 XX noctropic; transgenic; dermatitis; multiple sclerosis; diabetes mellitus;  
 XX allergy; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome;  
 XX osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological;  
 XX gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.

XX Homo sapiens.

XX WO2003050084-A2.

XX 19-JUN-2003.

XX 06-DEC-2002; 2002WO-US039126.

XX 07-DEC-2001; 2001US-0340235P.

XX 19-DEC-2001; 2001US-0343007P.

XX 21-DEC-2001; 2001US-0343546P.

XX 04-FEB-2002; 2002US-0354388P.

XX 15-FEB-2002; 2002US-0357675P.

XX (INCY-) INCYTE GENOMICS INC.

XX Kable AB, Chien D, Wilson AD, Swarnakar A, Gorrad AE;  
 PT Hafalia AJA, Smerling BM, Ramkumar J, Jin P, Griffin JA, Marguis UP;  
 PT Baughn WR, Chawla NK, Lehr-Mason PM, Khare R, Lee S, Hawkins PR;  
 PT Becha SD, Lee SY, Sprague WW, Zebajadlan Y;  
 DR WPI; 2003-532894/50.  
 XX N-FSDB; AAD57368.

XX New human kinases and phosphatases and polynucleotides, useful for  
 PT diagnosing, treating or preventing autoimmune or inflammatory disorders  
 PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,

cancer or hepatitis.

Claim 1; Page 243-244; 282pp; English.

The invention relates to an isolated polypeptide, which is a human kinase and phosphatase (KPP). KPP agonists and antagonists are useful for diagnosing, treating or preventing disorders associated with aberrant expression of KPP, particularly cell proliferative disorders (e.g., arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary chondrocytoma or cancer), developmental disorders (eg. renal tubular acidosis, anaemia or mental retardation), neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune/inflammatory disorders (e.g. AIDS, acquired immune deficiency syndrome, allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, gout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome, multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral, bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP is useful in assessing the effects of exogenous compounds on the expression of nucleic acids and kinases and phosphatases. KPP gene is useful in gene therapy and for creating transgenic animals to model human disease. The present sequence is human KPP protein

Sequence 412 AA:

Query Match: 4.1%; Score 19; DB 6; Length 412;  
Best Local Similarity 100.0%; Pred. No. 2.8e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

229 KNRREDILPYDSTRVPLGK 247  
|||||  
186 KNRREDILPYDSTRVPLGK 204

RESULT 13  
AAE14454  
ID AAE14454 standard; protein: 420 AA.  
XX AAE14454;  
AC  
XX  
DT 26-MAR-2002 (first entry)  
DS Human protein phosphatase-4.  
XX  
XX Human; protein phosphatase; PP-4; immune system disorder; AIDS; allergy;  
KW neurological disorder; developmental disorder; Alzheimer's disease;  
KW cell proliferative disorder; Huntington's disease; arteriosclerosis;  
KW renal tubular acidosis; gonadal dysgenesis; cancer; adenocarcinoma;  
KW leukaemia; transgenic animal; gene therapy.  
XX  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT Region 183..411  
FT /note="Protein-tyrosine phosphatase"  
FT Active-site 340..388  
FT /note="Tyrosine specific protein phosphatase active site"  
FT FT 351..363  
FT /note="Tyr\_phosphatase"  
FT FT 362..379  
FT Domain /label=Transmembrane\_domain  
XX  
PN WO200196546-A2.  
XX  
PD 20-DEC-2001.  
XX  
PF 14-JUN-2001; 2001WO-US019442.  
XX  
XX 16-JUN-2000; 2000US-0212447P.  
PR 22-JUN-2000; 2000US-0211746P.

PR		29-JUN-2000; 2000US-0215210P.
PR		06-JUN-2000; 2000US-0216529P.
FR		12-JUL-2000; 2000US-0218080P.
FR		21-JUN-2000; 2000US-0220117P.
XX		(INCY-) INCYTE GENOMICS INC.
PA		Au-Young J., Baughn MR., Ding L., Elliott VS., Gandhi AR., Griffin JA;
P1		Hafalla A., Kearney L., Lee RA., Lu Y., Nguyen DB., Patterson C;
P1		Rankumar J., Reddy R., Sanjwalwa MS., Stewart EA., Tang YT., Thornton M;
P1		Tribouley CC., Walla NK., Yang J., Yao MG., Yue H;
XX		WPI.; 2002-090206/12.
DR	N-PSDB:	AAD24022.
PT		Noxel polypeptide, useful for diagnosing, treating or preventing
PT		disorders of growth and development, immune system, neurological and cell
PT		proliferation diseases, comprises cancer protein phosphatase
PT		polypeptides.
PS		Claim 1; Page 105-106; 116pp; English.
XX		The present sequence is human protein phosphatase {pp}-4.. pp
CC		polynucleotide and polypeptide are useful in the diagnosis, treatment and
CC		prevention of immune system disorders, neurological disorders, Examples of
CC		developmental disorders and cell proliferative disorders. Examples of
CC		immune system disorders include acquired immune deficiency syndrome
CC		(AIDS), severe combined immunodeficiency disease (SCID), adult
CC		respiratory distress syndrome, allergies, amyloidosis, anaemia, asthma,
CC		atherosclerosis, Crohn's disease, atrophic dermatitis, diabetes mellitus,
CC		emphysema, Goodpasture's syndrome, gout, Graves' disease, multiple
CC		sclerosis, Myasthenia gravis, myocardial or pericardial inflammation,
CC		osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,
CC		rheumatoid arthritis, Sjogren's syndrome, scleroderma, systemic
CC		sclerosis, trauma; neurological disorders include Alzheimer's disease,
CC		Huntington's disease, dementia, epilepsy, Parkinson's disease, mental
CC		retardation and other developmental disorders of central nervous system
CC		such as Down's syndrome, cerebral palsy, periodic paralysis, mental
CC		disorders including mood, anxiety, and schizophrenia disorders, seasonal
CC		affective disorder such as akathisia, amnesia, cataplexy, dyskinesia;
CC		developmental disorders include e.g. renal tubular acidosis, Duchenne and
CC		Becker muscular dystrophy, gonadal dysgenesis, hypothyroidism; cell
CC		proliferative disorders include e.g. actinic keratosis, arteriosclerosis,
CC		atherosclerosis, bursitis, cirrhosis, hepatitis, psoriasis and cancer
CC		including adenocarcinoma, leukaemia. The polypeptide and polynucleotide
CC		are further useful for analysing a genome of a tissue or a cell type, for
CC		screening an agentist/antagonist, a compound that specifically binds to it
CC		or its modulator. The polynucleotide is useful for creating knock-in
CC		humanised animals (pigs) or transgenic animals (mice or rats) to model
CC		human disease, for generating a transcript image of a tissue or cell
CC		type, which represents the global pattern of gene expression by a
CC		particular tissue or cell type
XX		
SQ	Sequence	420 AA;
OY	Query March	4.1k; Score 19; DB 5; Length 420;
	Best Local Similarity	100.0%; Pred. No. 2.8e-10;
Mch	Matches 19; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Db		229 KRRYRDILPYDSTRVPLGK 247           186 KRRYRDILPYDSTRVPLGK 204
RESULT 14		
AD08106		AD08106 standard; protein; 508 AA.
AC	AD08106;	
DT	29-JAN-2004	(first entry)
DE		Novel protein (useful for identifying genetic disorders) #261.



GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: June 18, 2004, 19:46:09 ; Search time 23 Seconds

(without alignments)  
1039.253 Million cell updates/sec

Title: US-09-095-478a-6

Perfect score: 463

Sequence: 1 MSRRKRGKGTGRNDEBEG.....QYQPCIVLWLNLLALY 463

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/1aa/PCTUS.COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	3.2	272	US-08-446-345-34	Sequence 34, Appl
2	3.2	1174	US-08-446-345-36	Sequence 36, Appl
3	3.0	176	US-08-036-210-9	Sequence 9, Appl1
4	3.0	176	US-08-449-609-9	Sequence 9, Appl1
5	3.0	176	US-09-361-096A-9	Sequence 9, Appl1
6	3.0	245	US-08-685-992-26	Sequence 26, Appl
7	3.0	245	US-09-144-925-26	Sequence 26, Appl
8	3.0	289	US-09-361-096A-47	Sequence 47, Appl
9	3.0	322	US-08-036-210-11	Sequence 11, Appl
10	3.0	322	US-08-449-609-11	Sequence 11, Appl
11	3.0	322	US-09-361-096A-11	Sequence 11, Appl
12	3.0	401	US-09-361-096A-15	Sequence 15, Appl
13	3.0	402	US-08-036-210-15	Sequence 15, Appl
14	3.0	402	US-08-449-609-15	Sequence 15, Appl
15	3.0	898	US-08-036-210-22	Sequence 22, Appl
16	3.0	898	US-08-449-609-22	Sequence 22, Appl
17	3.0	898	US-09-361-096A-22	Sequence 22, Appl
18	3.0	1501	US-08-447-464-3	Sequence 3, Appl1
19	3.0	1501	US-08-716-679-3	Sequence 3, Appl1
20	3.0	1911	US-08-348-006B-5	Sequence 5, Appl1
21	3.0	1911	US-08-800-825A-5	Sequence 5, Appl1
22	3.0	1911	US-09-158-657-5	Sequence 5, Appl1
23	3.0	1911	PCT-US94-1016C-5	Sequence 5, Appl1
24	2.6	245	US-08-015-985-6	Sequence 6, Appl1
25	2.6	245	US-09-280-597-8	Sequence 8, Appl1
26	2.6	257	US-08-685-992-18	Sequence 18, Appl
27	2.6	257	US-09-144-925-18	Sequence 18, Appl

28	12	2.6	263	2	US-08-685-992-5	Sequence 5, Appl1
29	12	2.6	263	3	US-09-144-925-5	Sequence 5, Appl1
30	12	2.6	1337	3	US-08-854-585-2	Sequence 2, Appl1
31	12	2.6	1337	4	US-09-447-533-2	Sequence 2, Appl1
32	12	2.6	1337	5	PCT-US95-05512-2	Sequence 2, Appl1
33	12	2.6	1442	1	US-08-015-986A-3	Sequence 3, Appl1
34	12	2.6	1442	2	US-08-446-363-3	Sequence 3, Appl1
35	12	2.6	1445	1	US-08-015-986A-2	Sequence 2, Appl1
36	12	2.6	1445	2	US-08-446-363-2	Sequence 2, Appl1
37	12	2.6	1711	2	US-08-342-930-2	Sequence 2, Appl1
38	11	2.4	11	2	US-08-342-930-4	Sequence 4, Appl1
39	11	2.4	235	1	US-08-015-985-5	Sequence 5, Appl1
40	11	2.4	235	4	US-09-280-597-5	Sequence 5, Appl1
41	11	2.4	236	1	US-08-015-985-6	Sequence 6, Appl1
42	11	2.4	236	4	US-09-280-597-6	Sequence 6, Appl1
43	11	2.4	242	1	US-08-015-985-7	Sequence 7, Appl1
44	11	2.4	242	4	US-09-280-597-7	Sequence 7, Appl1
45	11	2.4	248	1	US-08-015-985-9	Sequence 9, Appl1

## ALIGNMENTS

RESULT 1  
US-08-446-345-34  
Sequence 34, Application US/08446345  
Patent No. 5831009  
GENERAL INFORMATION:  
APPLICANT: Ullrich, Axel  
APPLICANT: Moller, Niels P.H.  
APPLICANT: Moller, Karin B.  
TITLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE  
TITLE OF INVENTION: PHOSPHATASES PTP-D1  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: N.Y.  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,345  
FILING DATE: 22-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/234,440  
FILING DATE: 28-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Cotrucci, Laura A.  
REGISTRATION NUMBER: 30742  
REFERENCE/DOCKET NUMBER: 7683-054  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 272 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULAR TYPE: protein  
US-08-446-345-34  
Query Match 3.2%; Score 15; DB 2; Length 272;  
Best Local Similarity 100.0%; Pred. No. 1.4e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 391 PLVHCSAGVGRITGV 405  
 |||||  
 Db 201 PLVHCSAGVGRITGV 215

# RESULT 2

US-08-446-345-36  
 ; Sequence 36, Application US/08446345  
 ; Patent No. 5831009

## GENERAL INFORMATION:

APPLICANT: Ullrich, Axel  
 APPLICANT: Moller, Niels P.H.  
 APPLICANT: Moller, Karin B.  
 TITLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE  
 TITLE OF INVENTION: PHOSPHATASES PTP-D1  
 NUMBER OF SEQUENCES: 41  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: N.Y.

COUNTRY: U.S.A.  
 ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/446,345  
 FILING DATE: 22-MAY-1995  
 CLASSIFICATION: 435

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/234,440  
 FILING DATE: 28-APR-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A.  
 REGISTRATION NUMBER: 30742  
 REFERENCE/DOCKET NUMBER: 7683-054  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212)790-9090  
 TELEFAX: (212) 869-8864

## TELEFAX: (212) 869-8864

INFORMATION FOR SEQ ID NO: 36:  
 SEQUENCE CHARACTERISTICS:

LENGTH: 1174 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: unknown

TOPOLOGY: unknown  
 MOLECULE TYPE: protein

US-08-446-345-36

Query Match 3.2%; Score 15; DB 2; Length 1174;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 391 PLVHCSAGVGRITGV 405  
 |||||  
 Db 1103 PLVHCSAGVGRITGV 1117

US-08-036-210-9  
 ; Sequence 9, Application US/08036210  
 ; Patent No. 5585233

## GENERAL INFORMATION:

APPLICANT: Moller, Niels P.H.  
 APPLICANT: Moller, Karin B.  
 APPLICANT: Ullrich, Axel  
 TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE  
 TITLE OF INVENTION: PHOSPHATASE  
 NUMBER OF SEQUENCES: 45

## CORRESPONDENCE ADDRESS:

ADDRESSEE: PENNIE & EDMONDS  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/036,210  
 FILING DATE: 23-MAR-1993  
 CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

NAME: Mastrock, S. Leslie  
 REGISTRATION NUMBER: 18,872  
 REFERENCE/DOCKET NUMBER: 7683-025  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-790-9090  
 TELEFAX: 212-869-8864/9741

## TELEFAX: 212-869-8864/9741

INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:

LENGTH: 176 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein

US-08-036-210-9

Query Match 3.0%; Score 14; DB 1; Length 176;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 394 VHCASGVGRITGVPI 407  
 |||||  
 Db 79 VHCASGVGRITGVPI 92

US-08-449-609-9  
 ; Sequence 9, Application US/08449609  
 ; Patent No. 5952212

## GENERAL INFORMATION:

APPLICANT: Moller, Niels P.H.  
 APPLICANT: Moller, Karin B.  
 APPLICANT: Ullrich, Axel  
 TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE  
 TITLE OF INVENTION: PHOSPHATASE  
 NUMBER OF SEQUENCES: 45  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: PENNIE & EDMONDS  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York

COUNTRY: U.S.A.  
 ZIP: 10036-2711

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/449,609  
 FILING DATE: 24-MAY-1995  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/036,210  
 FILING DATE: 23-MAR-1993  
 ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7683-025  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8664/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 176 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-449-609-9

Query Match 3.0%; Score 14; DB 2; Length 176;  
Best Local Similarity 100.0%; Pred. No. 9.3e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 394 VHCAGVGRGTGVFI 407  
DB 79 VHCAGVGRGTGVFI 92

RESULT 5  
US-09-361-096A-9  
Sequence 9, Application US/09361096A  
Patent No. 6492495  
GENERAL INFORMATION:  
APPLICANT: MOLLER, NIELS P.H.  
APPLICANT: MOLLER, KARIN B.  
APPLICANT: ULARICH, AXEL  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE  
FILE REFERENCE: 038602/0686  
CURRENT APPLICATION NUMBER: US/09/361,096A  
CURRENT FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: 08/449,609  
PRIOR FILING DATE: 1995-05-24  
PRIOR APPLICATION NUMBER: 08/036,210  
PRIOR FILING DATE: 1995-03-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: Patentm Ver. 2.1  
SEQ ID NO 9  
LENGTH: 176  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: amino acid sequence  
US-09-361-096A-9

Query Match 3.0%; Score 14; DB 4; Length 176;  
Best Local Similarity 100.0%; Pred. No. 9.3e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 394 VHCAGVGRGTGVFI 407  
DB 79 VHCAGVGRGTGVFI 92

RESULT 6  
US-08-685-992-26  
Sequence 26, Application US/08685992  
Patent No. 5912138  
GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas  
APPLICANT: Flint, Andrew J.  
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,992  
FILING DATE: 25-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL96-03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 245 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-685-992-26

Query Match 3.0%; Score 14; DB 2; Length 245;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 394 VHCAGVGRGTGVFI 407  
DB 183 VHCAGVGRGTGVFI 196

RESULT 7  
US-09-144-925-26  
Sequence 26, Application US/09144925  
Patent No. 5951979  
GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas  
APPLICANT: Flint, Andrew J.  
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02421-4799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/144,925  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/685,992  
FILING DATE: JULY 25, 1996  
ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSH196-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 245 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-144-925-26

Query Match 3.0%; Score 14; DB 2; Length 245;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 394 VHCAGVGTGVFI 407  
DB 183 VHCAGVGTGVFI 196

RESULT 8  
US-09-361-096A-47  
Sequence 47, Application US/09361096A  
Patent No. 6492495  
GENERAL INFORMATION:  
APPLICANT: MOLLER, NIELS P.H.  
APPLICANT: MOLLER, KARIN B.  
APPLICANT: ULLRICH, AXEL  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE  
FILE REFERENCE: 038602/0686  
CURRENT FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: 08/449,609  
PRIOR FILING DATE: 1995-05-24  
PRIOR APPLICATION NUMBER: 08/036,210  
PRIOR FILING DATE: 1995-03-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 47  
LENGTH: 289  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: PTP-S31D  
US-09-361-096A-47

Query Match 3.0%; Score 14; DB 4; Length 289;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 394 VHCAGVGTGVFI 407  
DB 221 VHCAGVGTGVFI 234

RESULT 9  
US-08-036-210-11  
Sequence 11, Application US/08036210  
Patent No. 5585233  
GENERAL INFORMATION:  
APPLICANT: MOLLER, NIELS P.H.  
APPLICANT: MOLLER, KARIN B.  
APPLICANT: ULLRICH, AXEL  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE  
PHOSPHATASE  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS

STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/036,210  
FILING DATE: 23-MAR-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7683-025  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 322 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-036-210-11

Query Match 3.0%; Score 14; DB 1; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 394 VHCAGVGTGVFI 407  
DB 221 VHCAGVGTGVFI 234

RESULT 10  
US-08-449-609-11  
Sequence 11, Application US/08449609  
Patent No. 5952212  
GENERAL INFORMATION:  
APPLICANT: MOLLER, NIELS P.H.  
APPLICANT: MOLLER, KARIN B.  
APPLICANT: ULLRICH, AXEL  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE  
PHOSPHATASE  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/449,609  
FILING DATE: 24-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/036,210  
FILING DATE: 23-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872



REFERENCE/DOCKET NUMBER: 7663-025  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 322 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-443-609-11

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 394 VHCSAGVGRGVFI 407  
Db 221 VHCSAGVGRGVFI 234

RESULT 11  
US-09-361-096A-11  
Sequence 11, Application US/09361096A  
Patent No. 6492495  
GENERAL INFORMATION:  
APPLICANT: MOLLER, NIELS P.H.  
APPLICANT: MOLLER, KARIN B.  
APPLICANT: ULLRICH, AXEL  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE  
FILE REFERENCE: 038602/0686  
CURRENT APPLICATION NUMBER: US/09/361,096A  
CURRENT FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: 08/449,609  
PRIOR FILING DATE: 1995-05-24  
PRIOR APPLICATION NUMBER: 08/036,210  
PRIOR FILING DATE: 1995-03-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 11  
LENGTH: 322  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: PTP-S31D  
US-09-361-096A-11

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 394 VHCSAGVGRGVFI 407  
Db 221 VHCSAGVGRGVFI 234

RESULT 12  
US-09-361-096A-15  
Sequence 15, Application US/09361096A  
Patent No. 6492495  
GENERAL INFORMATION:  
APPLICANT: MOLLER, NIELS P.H.  
APPLICANT: MOLLER, KARIN B.  
APPLICANT: ULLRICH, AXEL  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE  
FILE REFERENCE: 038602/0686  
CURRENT APPLICATION NUMBER: US/09/361,096A  
CURRENT FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: 08/449,609  
PRIOR FILING DATE: 1995-05-24  
PRIOR APPLICATION NUMBER: 08/036,210

PRIOR FILING DATE: 1995-03-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 401  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-361-096A-15

Query Match  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 394 VHCSAGVGRGVFI 407  
Db 300 VHCSAGVGRGVFI 313

RESULT 13  
US-08-036-210-15  
Sequence 15, Application US/08036210  
Patent No. 5585233  
GENERAL INFORMATION:  
APPLICANT: MOLLER, NIELS P.H.  
APPLICANT: MOLLER, KARIN B.  
APPLICANT: ULLRICH, AXEL  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/036,210  
FILING DATE: 23-MAR-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7683-025  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 402 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-036-210-15

Query Match  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 394 VHCSAGVGRGVFI 407  
Db 301 VHCSAGVGRGVFI 314

RESULT 14  
US-08-443-609-15  
Sequence 15, Application US/08443609

Patent No. 55852212  
GENERAL INFORMATION:  
APPLICANT: Moller, Niels P.H.  
APPLICANT: Moller, Karin B.  
APPLICANT: Ullrich, Axel  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/449,609  
FILING DATE: 24-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/036,210  
FILING DATE: 23-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7683-025  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 402 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-449-609-15  
Query Match 3.0%; Score 14; DB 2; Length 402;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 394 VHCAGVGRGVPI 407  
DB 301 VHCAGVGRGVPI 314  
RESULT 15  
US-08-036-210-22  
Sequence 22, Application US/08036210  
Patent No. 5585233  
GENERAL INFORMATION:  
APPLICANT: Moller, Niels P.H.  
APPLICANT: Moller, Karin B.  
APPLICANT: Ullrich, Axel  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/036,210  
FILING DATE: 23-MAR-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7683-025  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 898 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-036-210-22  
Query Match 3.0%; Score 14; DB 1; Length 898;  
Best Local Similarity 100.0%; Pred. No. 4.3e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 394 VHCAGVGRGVPI 407  
DB 797 VHCAGVGRGVPI 810  
Search completed: June 18, 2004, 19:49:51  
Job time : 23 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:48:50 ; Search time 48 Seconds  
(without alignments)  
2723.150 Million cell updates/sec

Title: US-09-095-478a-6  
Perfect score: 463

Sequence: 1 MSFPRKVRGKTGRNDREGE.....QYCFEIVLEVLQNLALY 463

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1163542 segs, 28233646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/2/pubpaa/PC7\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PC7US\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
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- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_NEW\_PUB.pep.\*
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- 14: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
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- 16: /cgn2\_6/ptodata/2/pubpaa/US10C\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	463	100.0	463	10	US-09-095-478-2
2	383	82.7	426	10	US-09-095-478-1
3	379	81.9	379	10	US-09-095-478-8
4	362	78.2	412	10	US-09-095-478-3
5	354	76.5	354	10	US-09-095-478-6
6	122	26.3	122	10	US-09-095-478-4
7	30	6.3	30	10	US-09-095-478-22
8	29	6.3	29	10	US-09-095-478-23
9	29	6.3	29	10	US-09-095-478-24
10	29	6.3	29	10	US-09-095-478-25
11	23	5.0	122	10	US-09-095-478-5
12	19	4.1	420	16	US-10-311-764-4
13	15	3.2	1105	12	US-10-396-115-1082
14	14	3.0	162	15	US-10-334-143-191
15	14	3.0	176	14	US-10-314-232-9

16	14	3.0	289	14	US-10-314-232-47	Sequence 47, Appl
17	14	3.0	294	9	US-09-788-626-27	Sequence 27, Appl
18	14	3.0	322	14	US-10-314-232-11	Sequence 11, Appl
19	14	3.0	344	16	US-10-408-765A-1670	Sequence 1670, Ap
20	14	3.0	401	14	US-10-314-232-15	Sequence 150, Appl
21	14	3.0	442	9	US-09-925-300-950	Sequence 950, App
22	14	3.0	647	15	US-10-291-265-722	Sequence 722, Appl
23	14	3.0	898	14	US-10-314-232-22	Sequence 22, Appl
24	14	3.0	1495	15	US-10-258-666-12	Sequence 12, Appl
25	14	3.0	1502	9	US-09-808-602-54	Sequence 54, Appl
26	14	3.0	1502	10	US-09-800-198-44	Sequence 44, Appl
27	14	3.0	1907	15	US-10-291-265-250	Sequence 250, Appl
28	14	3.0	1948	9	US-09-808-602-55	Sequence 55, Appl
29	14	3.0	1948	10	US-09-800-198-45	Sequence 45, Appl
30	14	3.0	2281	12	US-10-087-684-6	Sequence 6, Appl
31	14	3.0	2281	14	US-10-218-779-6	Sequence 6, Appl
32	14	3.0	2291	10	US-09-822-871-2	Sequence 2, Appl
33	14	3.0	2291	16	US-10-673-885-2	Sequence 2, Appl
34	14	3.0	2299	16	US-10-466-755-2	Sequence 2, Appl
35	14	3.0	2300	12	US-10-087-684-10	Sequence 10, Appl
36	14	3.0	2300	12	US-10-218-779-10	Sequence 10, Appl
37	14	3.0	2301	10	US-09-822-871-4	Sequence 4, Appl
38	14	3.0	2301	16	US-10-673-885-4	Sequence 4, Appl
39	14	3.0	2302	12	US-10-087-684-37	Sequence 37, Appl
40	14	3.0	2302	12	US-10-218-779-37	Sequence 37, Appl
41	12	2.6	313	9	US-09-788-626-19	Sequence 19, Appl
42	12	2.6	319	9	US-09-788-626-6	Sequence 6, Appl
43	12	2.6	1216	15	US-10-366-547-49	Sequence 49, Appl
44	12	2.6	1238	15	US-10-366-547-47	Sequence 47, Appl
45	12	2.6	1329	16	US-10-408-765A-2747	Sequence 2747, Ap

## ALIGNMENTS

RESULT 1  
US-09-095-478-2  
Sequence 2, Application US/09095478  
Publication No. US20030095970A1  
GENERAL INFORMATION:  
APPLICANT: Plowman, Gregory  
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE SUPTOS AND  
TITLE OF INVENTION: RELATED PRODUCTS AND  
METHODS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FASTSEQ for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/095,478  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 224/115  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 463 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-09-095-478-2

Query Match 100.0%; Score 463; DB 10; Length 463;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 463; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSPKRGKGTGRDDEEGNSGNLNLNPLSSSQKTPPKPQNRNLMKYEELHILM 60  
DB 1 MSSPKRGKGTGRDDEEGNSGNLNLNPLSSSQKTPPKPQNRNLMKYEELHILM 60  
QY 61 VFLIKITWYVFKLMKGLIFGNKNSENVKPSHHLSFSDKYELVPEPLESDTDETW 120  
DB 61 VFLIKITWYVFKLMKGLIFGNKNSENVKPSHHLSFSDKYELVPEPLESDTDETW 120  
QY 121 DVSDBSLNRNNSDSETAGPSKTVSPVLSGSSRLSKDTETSVSEKELTQIAQIRPLEN 180  
DB 121 DVSDBSLNRNNSDSETAGPSKTVSPVLSGSSRLSKDTETSVSEKELTQIAQIRPLEN 180  
QY 181 SSASARAMDCLNTLOKKEELDIIRFELBLEQMTLPDDFNSGNTLQNRDKNRYDILPYDS 240  
DB 181 SSASARAMDCLNTLOKKEELDIIRFELBLEQMTLPDDFNSGNTLQNRDKNRYDILPYDS 240  
QY 241 TRVPLGKNDYINASYIRIVNHEEYFYIAQGPLPETIEDPWQMTLNNCNVIAMTRE 300  
DB 241 TRVPLGKNDYINASYIRIVNHEEYFYIAQGPLPETIEDPWQMTLNNCNVIAMTRE 300  
QY 301 IECGVKCYSPWISLKEPLEPEHPSVLEFHTVQYFVAVFOIVKSKSGCVKHLQ 360  
DB 301 IECGVKCYSPWISLKEPLEPEHPSVLEFHTVQYFVAVFOIVKSKSGCVKHLQ 360  
QY 361 FTKWPDHGTSPASADFFIKYRVYRKSHITGPILVHCSAGVGTGVCVAVPSAIEKNY 420  
DB 361 FTKWPDHGTSPASADFFIKYRVYRKSHITGPILVHCSAGVGTGVCVAVPSAIEKNY 420  
QY 421 SFDINIVTQMRKQRCGMIOFTEQYQFCYEIVLEVLQNLALY 463  
DB 421 SFDINIVTQMRKQRCGMIOFTEQYQFCYEIVLEVLQNLALY 463

## RESULT 2

US-09-095-478-1  
Sequence 1, Application US/0905478  
Publication No. US20030095970A1  
GENERAL INFORMATION:  
APPLICANT: PLOWMAN, Gregory  
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE SUPPOS AND  
TITLE OF INVENTION: RELATED PRODUCTS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/095,478  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 224/115  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 469-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 426 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-09-095-478-1

Query Match 82.7%; Score 383; DB 10; Length 426;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 44 IFGNKNSENVKPSHHLSFSDKYELVPEPLESDTDETWVSDRSIRNNSDSETAG 103  
QY 141 PSKTVSPVLSGSSRLSKDTETSVSEKELTQIAQIRPLENNSARAMDCLNTLOKKEEL 200  
DB 104 PSKTVSPVLSGSSRLSKDTETSVSEKELTQIAQIRPLENNSARAMDCLNTLOKKEEL 163  
QY 201 DIREFLEBLEQMTLPDDFNSGNTLQNRDKNRYDILPYDSTRVPLGKNDYINASYIRIV 260  
DB 164 DIREFLEBLEQMTLPDDFNSGNTLQNRDKNRYDILPYDSTRVPLGKNDYINASYIRIV 223  
QY 261 NHEEYFYIAQGPLPETIEDPWQMTLNNCNVIAMTREIEGVKCYSPWISLKEPL 320  
DB 224 NHEEYFYIAQGPLPETIEDPWQMTLNNCNVIAMTREIEGVKCYSPWISLKEPL 283  
QY 321 EFHFPSVLEFHTVQYFVAVFOIVKSKSGCVKHLQFTKMPDHGTSPASADFFIKYV 380  
DB 284 EFHFPSVLEFHTVQYFVAVFOIVKSKSGCVKHLQFTKMPDHGTSPASADFFIKYV 343  
QY 381 RYVRSKSHITGPILVHCSAGVGTGVCVAVPSAIEKNYSFDINIVTQMRKQRCGMIO 440  
DB 344 RYVRSKSHITGPILVHCSAGVGTGVCVAVPSAIEKNYSFDINIVTQMRKQRCGMIO 403  
QY 441 TREQYQFCYEIVLEVLQNLALY 463  
DB 404 TREQYQFCYEIVLEVLQNLALY 426

## RESULT 3

US-09-095-478-8  
Sequence 8, Application US/0905478  
Publication No. US20030095970A1  
GENERAL INFORMATION:  
APPLICANT: PLOWMAN, Gregory  
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE SUPPOS AND  
TITLE OF INVENTION: RELATED PRODUCTS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles

STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071-2066  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FastSeq for Windows 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/095,478  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard J.  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 224/115  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 379 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 US-09-095-478-8

Query Match 81.9%; Score 379; DB 10; Length 379;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 GNKNSENVKPSHLSFSDKELYPPLESDTDETVWDVSDRLRRNMSMDSETAGPS 142  
 DB 1 GNKNSENVKPSHLSFSDKELYPPLESDTDETVWDVSDRLRRNMSMDSETAGPS 60  
 QY 143 KTVSPVLSGSSRLSKDTETSVSEKELTQLAQIRPLINSSARSAARDCLNTLQKKEELDI 202  
 DB 61 KTVSPVLSGSSRLSKDTETSVSEKELTQLAQIRPLINSSARSAARDCLNTLQKKEELDI 120  
 QY 203 IREFLELQOMTLPPDPFNSGNTLQNRDKRYDILPYDSTRVPLGKNKOYINASTYIRIVN 262  
 DB 121 IREFLELQOMTLPPDPFNSGNTLQNRDKRYDILPYDSTRVPLGKNKOYINASTYIRIVN 180  
 QY 263 EEEFYIATQGPLDETIEDFWOMYLENNCNVIAITREIECGVIKCYSYWPISLKEPLEF 322  
 DB 181 EEEFYIATQGPLDETIEDFWOMYLENNCNVIAITREIECGVIKCYSYWPISLKEPLEF 240  
 QY 323 EHFSPVLETFTHTVQYFTYRVFOIVKSGSKOCYKHLOFTWPHGTPASADFTIKYVY 382  
 DB 241 EHFSPVLETFTHTVQYFTYRVFOIVKSGSKOCYKHLOFTWPHGTPASADFTIKYVY 300  
 QY 383 VRKSHITGPLLVHSGAGVGRGVFLCYDVVSALEKNYSPDINNIIVTQMRKQRCGMIOQTK 442  
 DB 301 VRKSHITGPLLVHSGAGVGRGVFLCYDVVSALEKNYSPDINNIIVTQMRKQRCGMIOQTK 360  
 QY 443 EOYQFCIEIVLEVLQNLILA 461  
 DB 361 EOYQFCIEIVLEVLQNLILA 379

#### RESULT 4

US-09-095-478-3  
 Sequence 3, Application US/09095478  
 Publication No. US2003009570A1  
 GENERAL INFORMATION:  
 APPLICANT: Plozman, Gregory  
 TITLE OF INVENTION: NOVEL PROTEIN TYROSINE

TITLE OF INVENTION: PHOSPHATASE SUPPROS AND  
 TITLE OF INVENTION: RELATED PRODUCTS AND  
 TITLE OF INVENTION: METHODS  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071-2066  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FastSeq for Windows 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/095,478  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard J.  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 224/115  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 412 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 US-09-095-478-3

Query Match 78.2%; Score 362; DB 10; Length 412;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 IFGNKNSENVKPSHLSFSDKELYPPLESDTDETVWDVSDRLRRNMSMDSETAG 140  
 DB 44 IFGNKNSENVKPSHLSFSDKELYPPLESDTDETVWDVSDRLRRNMSMDSETAG 103  
 QY 141 PSKTVSPVLSGSSRLSKDTETSVSEKELTQLAQIRPLINSSARSAARDCLNTLQKKEEL 200  
 DB 104 PSKTVSPVLSGSSRLSKDTETSVSEKELTQLAQIRPLINSSARSAARDCLNTLQKKEEL 163  
 QY 201 DIREFLELQOMTLPPDPFNSGNTLQNRDKRYDILPYDSTRVPLGKNKOYINASTYIRIV 260  
 DB 164 DIREFLELQOMTLPPDPFNSGNTLQNRDKRYDILPYDSTRVPLGKNKOYINASTYIRIV 223  
 QY 261 NHEEYFYIATQGPLDETIEDFWOMYLENNCNVIAITREIECGVIKCYSYWPISLKEPLE 320  
 DB 224 NHEEYFYIATQGPLDETIEDFWOMYLENNCNVIAITREIECGVIKCYSYWPISLKEPLE 283  
 QY 321 EHFSPVLETFTHTVQYFTYRVFOIVKSGSKOCYKHLOFTWPHGTPASADFTIKYVY 380  
 DB 284 EHFSPVLETFTHTVQYFTYRVFOIVKSGSKOCYKHLOFTWPHGTPASADFTIKYVY 343  
 QY 381 RYVRKSHITGPLLVHSGAGVGRGVFLCYDVVSALEKNYSPDINNIIVTQMRKQRCGMIO 440  
 DB 344 RYVRKSHITGPLLVHSGAGVGRGVFLCYDVVSALEKNYSPDINNIIVTQMRKQRCGMIO 403  
 QY 441 TK 442  
 DB 404 TK 405

RESULT 5  
US-09-095-478-6  
Sequence 6, Application US/09095478  
Publication No. US20030095970A1  
GENERAL INFORMATION:  
APPLICANT: Plowman, Gregory  
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE SUPP05 AND  
TITLE OF INVENTION: RELATED PRODUCTS AND  
METHODS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/095,478  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 224/115  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 354 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-09-095-478-6

Query Match 76.5%; Score 354; DB 10; Length 354;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 PEPESDIDETVMDVSDRLNRNWSMDSEIAPGSKTVSPVLSSGSSRLSKOTETVSSEKE 167  
DB 1 PEPESDIDETVMDVSDRLNRNWSMDSEIAPGSKTVSPVLSSGSSRLSKOTETVSSEKE 60

QY 168 LITOLAQIFPLFNSARSARAMDCLNTLOKKEELDIIRFLEBOMTLDPDPSANTLONR 227  
DB 61 LITOLAQIFPLFNSARSARAMDCLNTLOKKEELDIIRFLEBOMTLDPDPSANTLONR 120

QY 228 DKNRRDILFPLFNSARSARAMDCLNTLOKKEELDIIRFLEBOMTLDPDPSANTLONR 287  
DB 121 DKNRRDILFPLFNSARSARAMDCLNTLOKKEELDIIRFLEBOMTLDPDPSANTLONR 180

QY 288 ENNCNVAMITREIEGVIKCYSTWPISLKEPLSEHVSFLFTHVQYTVAVRQIVK 347  
DB 181 ENNCNVAMITREIEGVIKCYSTWPISLKEPLSEHVSFLFTHVQYTVAVRQIVK 240

QY 348 KSTGSKQCVKHLQFTKMPDHGTASADFFIKYRVYRKSHITGPILVHCSAGVGTGTFPI 407

DB 241 KSTGSKQCVKHLQFTKMPDHGTASADFFIKYRVYRKSHITGPILVHCSAGVGTGTFPI 300

QY 408 CVDVPSAIEKNYSFDIMNITVONKROKRCMIQTEKOYQFCYEIVLEVLQNLIA 461  
DB 301 CVDVPSAIEKNYSFDIMNITVONKROKRCMIQTEKOYQFCYEIVLEVLQNLIA 354

RESULT 6  
US-09-095-478-4  
Sequence 4, Application US/09095478  
Publication No. US20030095970A1  
GENERAL INFORMATION:  
APPLICANT: Plowman, Gregory  
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE SUPP05 AND  
TITLE OF INVENTION: RELATED PRODUCTS AND  
METHODS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/095,478  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 224/115  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-09-095-478-4

Query Match 26.3%; Score 122; DB 10; Length 122;  
Best Local Similarity 100.0%; Pred. No. 1.6e-112;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 DFMQVLENNCNVIAITREIEGVIKCYSTWPISLKEPLSEHVSFLFTHVQYTV 340  
DB 1 DFMQVLENNCNVIAITREIEGVIKCYSTWPISLKEPLSEHVSFLFTHVQYTV 60

QY 341 RVFOIVKSTGSKQCVKHLQFTKMPDHGTASADFFIKYRVYRKSHITGPILVHCSAGV 400  
DB 61 RVFOIVKSTGSKQCVKHLQFTKMPDHGTASADFFIKYRVYRKSHITGPILVHCSAGV 120

QY 401 GR 402  
DB 121 GR 122

```
RESULT 7
US-09-095-478-22
; Sequence 22, Application US/09095478
; Publication No. US20030095970A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND
; TITLE OF INVENTION: RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-09-095-478-22

Query Match 6.5%; Score 30; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 7.8e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 213 TLPPDFNSGNTLQNDKRYRDILPYDSTR 242
DB 1 TLPPDFNSGNTLQNDKRYRDILPYDSTR 30

RESULT 8
US-09-095-478-23
; Sequence 23, Application US/09095478
; Publication No. US20030095970A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND
; TITLE OF INVENTION: RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-09-095-478-23
```

```
QY 1 MSSPRKVRGKTGRDNDDEBGSNGLNLRN 29
DB 1 MSSPRKVRGKTGRDNDDEBGSNGLNLRN 29

RESULT 9
US-09-095-478-24
; Sequence 24, Application US/09095478
; Publication No. US20030095970A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND
; TITLE OF INVENTION: RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-09-095-478-23

Query Match 6.3%; Score 29; DB 10; Length 29;
Best Local Similarity 100.0%; Pred. No. 7.4e-21;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSPRKVRGKTGRDNDDEBGSNGLNLRN 29
DB 1 MSSPRKVRGKTGRDNDDEBGSNGLNLRN 29
```

APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 224/115  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-09-095-478-24

Query Match 6.3%; Score 29; DB 10; Length 29;  
Best Local Similarity 100.0%; Pred. No. 7.4e-21;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 146 SPVLSSSRSLSKDPTSYSEKELTQLAOI 174  
Db 1 SPVLSSSRSLSKDPTSYSEKELTQLAOI 29

RESULT 10  
US-09-095-478-25  
Sequence 25, Application US/09095478  
Publication No. US20030095970A1  
GENERAL INFORMATION:  
APPLICANT: PLOWMAN, Gregory  
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE SUPPOS AND  
TITLE OF INVENTION: RELATED PRODUCTS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
CLASSIFICATION:  
ADDRESS: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FASTSEQ for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/095,478  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 224/115  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-09-095-478-25

Query Match 6.3%; Score 29; DB 10; Length 29;  
Best Local Similarity 100.0%; Pred. No. 7.4e-21;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 120 MDVSDRLRRNRMNSDSTAGPSKTVSPV 148  
Db 1 MDVSDRLRRNRMNSDSTAGPSKTVSPV 29

RESULT 11  
US-09-095-478-5  
Sequence 5, Application US/09095478  
Publication No. US20030095970A1  
GENERAL INFORMATION:

APPLICANT: PLOWMAN, Gregory  
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE SUPPOS AND  
TITLE OF INVENTION: RELATED PRODUCTS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
CLASSIFICATION:  
ADDRESS: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FASTSEQ for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/095,478  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 224/115  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-09-095-478-5

Query Match 5.0%; Score 23; DB 10; Length 122;  
Best Local Similarity 100.0%; Pred. No. 2.4e-14;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 374 DPEIKYVRYVRKSHITGPPLVHC 396  
Db 94 DPEIKYVRYVRKSHITGPPLVHC 116

RESULT 12  
US-10-311-764-4



Sequence 4, Application US/10311764  
Publication No. US20040023245A1  
GENERAL INFORMATION:  
APPLICANT: INCYTE GENOMICS, INC.; AU-YOUNG, Janice K.  
APPLICANT: BAUGHN, Mariah R.; DING, Li  
APPLICANT: ELLIOTT, Vicki S.; GANDHI, Aarena R.  
APPLICANT: GRIFFIN, Jennifer A.; HARALIN, April J.A.  
APPLICANT: KEARNEY, Liam; LEE, Ernestine A.  
APPLICANT: LO, Yan; NGUYEN, Daniel B.  
APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi  
APPLICANT: REDDY, Roopa M.; SANJAYWALA, Madhusudan M.  
APPLICANT: STEWART, Elizabeth A.; TANG, Y. Tom  
APPLICANT: THORNTON, Michael B.; TRIBOUTY, Catherine M.  
APPLICANT: CHAKRA, Narinder K.; YANG, Henry  
APPLICANT: YAO, Montyue G.; YUE, Henry  
TITLE OF INVENTION: PROTEIN PHOSPHATASES  
FILE REFERENCE: PI-0126 USN  
CURRENT APPLICATION NUMBER: US/10/311,764  
CURRENT FILING DATE: 2002-12-16  
PRIOR APPLICATION NUMBER: PCT/US01/19442  
PRIOR FILING DATE: 2001-06-14  
PRIOR APPLICATION NUMBER: US 60/212,447  
PRIOR FILING DATE: 2000-06-16  
PRIOR APPLICATION NUMBER: US 60/213,746  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: US 60/215,210  
PRIOR FILING DATE: 2000-06-29  
PRIOR APPLICATION NUMBER: US 60/216,529  
PRIOR FILING DATE: 2000-07-06  
PRIOR APPLICATION NUMBER: US 60/218,080  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/220,117  
PRIOR FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PERL Program  
SEQ ID NO 4  
LENGTH: 420  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. US20040023245A1 7476861CD1  
US-10-311-764-4  
Query Match 4.1%; Score 19; DB 16; Length 420;  
Best Local Similarity 100.0%; Pred. No. 6.8e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 229 KNRFDILPDSGRVPLGK 247  
DB 186 KNRFDILPDSGRVPLGK 204  
RESULT 13  
US-10-296-115-1082  
Sequence 1082, Application US/10296115  
Publication No. US20040053248A1  
GENERAL INFORMATION:  
APPLICANT: Hyseq Inc  
TITLE OF INVENTION: No. US20040053248A1 Nucleic Acids and Polypeptides  
FILE REFERENCE: 784PCT  
CURRENT APPLICATION NUMBER: US/10/296,115  
CURRENT FILING DATE: 2002-11-18  
PRIOR APPLICATION NUMBER: US09/488,725  
PRIOR FILING DATE: 2000-01-21  
PRIOR APPLICATION NUMBER: US09/552,317  
PRIOR FILING DATE: 2000-04-25  
NUMBER OF SEQ ID NOS: 1478  
SEQ ID NO 1082  
LENGTH: 1105  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:

NAME/KEY: misc feature  
LOCATION: (1) ... (1105)  
OTHER INFORMATION: Xaa = any amino acid or other as shown in Table 3  
US-10-296-115-1082  
Query Match 3.2%; Score 15; DB 12; Length 1105;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 391 PLVHCSAGVGRGV 405  
DB 1015 PLVHCSAGVGRGV 1029  
RESULT 14  
US-10-334-143-191  
Sequence 191, Application US/10334143  
Publication No. US20040009549A1  
GENERAL INFORMATION:  
APPLICANT: GRIGORIY, IGOR VYACHESLAVOVICH  
APPLICANT: SUDARSANAM, SUCHA  
TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL  
TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD  
FILE REFERENCE: 038602/1543  
CURRENT APPLICATION NUMBER: US/10/334,143  
CURRENT FILING DATE: 2002-12-31  
PRIOR APPLICATION NUMBER: 60/343,169  
PRIOR FILING DATE: 2001-12-31  
NUMBER OF SEQ ID NOS: 207  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 191  
LENGTH: 162  
TYPE: PRT  
ORGANISM: Unknown Organism  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: 11ara protein sequence  
US-10-334-143-191  
Query Match 3.0%; Score 14; DB 15; Length 162;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 394 VHCASGVGRGV 407  
DB 103 VHCASGVGRGV 116  
RESULT 15  
US-10-314-232-9  
Sequence 9, Application US/10314232  
Publication No. US20030138932A1  
GENERAL INFORMATION:  
APPLICANT: MOLLER, NIELS P.H.  
APPLICANT: MOLLER, KARIN B.  
APPLICANT: ULRICH, AXEL  
TITLE OF INVENTION: PTP-S21: A NOVEL PROTEIN TYROSINE PHOSPHATASE  
FILE REFERENCE: 038602/0686  
CURRENT APPLICATION NUMBER: US/10/314,232  
CURRENT FILING DATE: 2002-12-09  
PRIOR APPLICATION NUMBER: US/09/361,096  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: 08/449,609  
PRIOR FILING DATE: 1995-05-24  
PRIOR APPLICATION NUMBER: 08/036,210  
PRIOR FILING DATE: 1995-03-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 9  
LENGTH: 176  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: amino acid sequence

OTHER INFORMATION: encoded by PCR fragment  
US-10-314-232-9

Query Match: 3.0%; Score 14; DB 14; Length 176;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 394 VHCAGVGRITGVFI 407  
|||  
Db 79 VHCAGVGRITGVFI 92

Search completed: June 18, 2004, 19:54:43  
Job time : 49 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:45:04 ; Search time 21 Seconds  
(without alignments)  
2120.794 Million cell updates/sec

Title: US-09-095-478a-6

Perfect score: 453

Sequence: 1 MSSPRKVRKGTGRDNDEEG.....QYQFCYHLYLVLIQNTLALY 463

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : PIR 78:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	4.1	398	2 T08716	protein-tyrosine-p
2	15	3.2	1174	2 I38140	protein-tyrosine-p
3	15	3.2	1175	2 S51005	protein-tyrosine-p
4	15	3.2	1176	2 I58345	protein-tyrosine-p
5	14	3.0	582	2 A57068	protein-tyrosine-p
6	14	3.0	1231	2 S53089	protein-tyrosine-p
7	14	3.0	1290	2 A56493	leucocyte common a
8	14	3.0	1496	1 A48758	protein-tyrosine-p
9	14	3.0	1499	2 I50212	protein-tyrosine-p
10	14	3.0	1501	2 I58148	protein-tyrosine-p
11	14	3.0	1691	1 D54689	protein-tyrosine-p
12	14	3.0	1863	2 S46217	protein-tyrosine-p
13	14	3.0	1894	2 C54689	protein-tyrosine-p
14	14	3.0	1897	1 TDHUK	leukocyte antigen-
15	14	3.0	1898	1 S46216	leukocyte antigen-
16	14	3.0	1907	2 S50893	protein-tyrosine-p
17	14	3.0	1912	2 A56178	protein-tyrosine-p
18	14	3.0	2051	2 T30938	receptor tyrosine
19	14	3.0	2302	2 T14328	protein-tyrosine-p
20	14	2.6	184	2 T15125	hypothetical prote
21	12	2.6	1187	1 UC4155	protein-tyrosine-p
22	12	2.6	1189	1 UC2366	protein-tyrosine-p
23	12	2.6	1217	2 T22672	hypothetical prote
24	12	2.6	1238	2 S68700	HTP beta-like tyr
25	12	2.6	1337	1 I38470	protein-tyrosine-p
26	12	2.6	1442	1 B48148	protein-tyrosine-p
27	12	2.6	1445	1 A48148	protein-tyrosine-p
28	12	2.6	1462	1 B36182	protein-tyrosine-p
29	12	2.6	1711	1 A55148	protein-tyrosine-p

30	11	2.4	198	2 T27722	hypothetical prote
31	11	2.4	356	2 A40169	protein-tyrosine-p
32	11	2.4	355	1 A39862	protein-tyrosine-p
33	11	2.4	398	2 I56540	protein-tyrosine-p
34	11	2.4	405	2 I49372	protein-tyrosine-p
35	11	2.4	405	2 S68250	protein-tyrosine-p
36	11	2.4	483	2 T25982	hypothetical prote
37	11	2.4	521	1 A44267	protein-tyrosine-p
38	11	2.4	550	1 A40449	protein-tyrosine-p
39	11	2.4	583	2 S17671	protein-tyrosine-p
40	11	2.4	699	2 UC6132	protein-tyrosine-p
41	11	2.4	700	1 S12053	protein-tyrosine-p
42	11	2.4	711	1 S28391	protein-tyrosine-p
43	11	2.4	796	1 UC1285	protein-tyrosine-p
44	11	2.4	802	1 A36065	protein-tyrosine-p
45	11	2.4	829	1 A47373	protein-tyrosine-p

#### ALIGNMENTS

RESULT 1  
T08716  
protein-tyrosine-phosphatase homolog DKFZp566K0524.1 - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 13-Aug-1999  
C/Accession: T08716  
R/Annotg, W.: Winkler, U.; Mewer, H.W.; Gassenhuber, J.; Wilmann, S.  
submitted to the Protein Sequence Database, May 1999  
A/Reference number: Z16472  
A/Accession: T08716  
A/Molecule type: mRNA  
A/Residues: 1-398 <RNA>  
A/Cross-references: EMBL:AL050040  
A/Experimental source: fetal kidney; clone DKFZp566K0524  
C/Genetics:  
A/Note: DKFZp566K0524.1  
C/Superfamily: protein-tyrosine-phosphatase homology  
F:161-379/Domain: protein-tyrosine-phosphatase homology <PTP>

Query Match 4.1%; Score 19; DB 2; Length 398;  
Best Local Similarity 100.0%; Pred. No. 4e-11;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 KNRKRDILPYDSTRVPLGK 247  
Db 164 KNRKRDILPYDSTRVPLGK 182

RESULT 2  
I38140  
protein-tyrosine-phosphatase (EC 3.1.3.48) - human  
C/Species: Homo sapiens (man)  
C/Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 22-Jun-1999  
C/Accession: I38140  
R/Moller, N.P.; Moller, K.B.; Lammerig, R.; Khartonenkov, A.; Sures, I.; Ulrich, A.  
Proc. Natl. Acad. Sci. U.S.A. 91, 7477-7481, 1994  
A/Title: Src kinase associates with a member of a distinct subfamily of protein-tyrosin  
A/Reference number: I38140; MUID:94329538; PMID:7519780  
A/Accession: I38140  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-1174 <RES>  
A/Cross-references: EMBL:X79510; NID:G532055; PIDN:CA56042.1; PID:G532056  
C/Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-  
C/Keyword: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphata  
F:25-304/Domain: protein 4.1 membrane-binding domain homology <B41>  
F:321-1156/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F:1108/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1114/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.2%; Score 15; DB 2; Length 1174;  
Best Local Similarity 100.0%; Pred. No. 1.5e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 PLVHCSAGVGRGV 405  
 |||||

Db 1103 PLVHCSAGVGRGV 1117

#### RESULT 3

S51005

protein-tyrosine-phosphatase (EC 3.1.3.48) 2E - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 10-Apr-1996 #sequence\_revision 03-May-1996 #text\_change 22-Jun-1999

C/Accession: S51005; S51161

R/L/Abbe, D.; Banville, D.; Tong, Y.; Stocco, R.; Masson, S.; Ma, S.; Fantus, G.; Shen,

FEBS Lett. 356, 351-356, 1994

A/Title: Identification of a novel protein tyrosine phosphatase with sequence homology to

A/Reference number: S51005; MUID:95104449; PMID:7805871

A/Accession: S51005

A/Molecule type: mRNA

A/Residues: 1-1175 <LAA>

A/Cross-references: EMBL:U19771; NID:G662113; PIDN:AAA62153.1; PID:G602255

A/Genetics: PTP2B

A/Accession: S51161

A/Molecule type: mRNA

A/Residues: 840-1175 <LAB>

A/Cross-references: EMBL:U18293; NID:G603228; PIDN:AAA62154.1; PID:G603229

A/Genetics: PTP2E1

C/Genetics: <PTP2B>

A/Note: clone PTP2E1

C/Genetics: <PTP2E1>

A/Note: clone PTP2E1

C/Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-t

C/Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase

F/25-304/Domain: protein 4.1 membrane-binding domain homology <B41>

F/922-1157/Domain: protein-tyrosine-phosphatase homology <PTP2>

F/1109/Active site: Cys (phosphocysteine intermediate) #status predicted

F/1115/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.2%; Score 15; DB 2; Length 1175;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 PLVHCSAGVGRGV 405  
 |||||

Db 1104 PLVHCSAGVGRGV 1118

#### RESULT 4

S58345

protein tyrosine phosphatase - mouse

C/Species: Mus musculus (house mouse)

C/Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 22-Jun-1999

C/Accession: S58345

R/Higashitsuji, H.; Arai, S.; Furutani, M.; Imanura, M.; Kaneko, Y.; Takenawa, T.; Nakay

Ono, M.; Ohtsuka, T.; Saito, Y.

A/Title: Enhanced expression of multiple protein tyrosine phosphatases in the regenerat

A/Reference number: S58345; MUID:95140431; PMID:7838537

A/Accession: S58345

A/Molecule type: mRNA

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Residues: 1-1176 <RES>

A/Cross-references: GB:D37801; NID:G604885; PIDN:BAA07053.1; PID:G604886

C/Genetics: PTP-RL10

A/Genetics: PTP-RL10

C/Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-t

C/Keywords: phosphoprotein

F/25-304/Domain: protein 4.1 membrane-binding domain homology <B41>

F/923-1158/Domain: protein-tyrosine-phosphatase homology <PTP2>

F/1110/Active site: Cys (phosphocysteine intermediate) #status predicted

F/1116/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.2%; Score 15; DB 2; Length 1176;

Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 PLVHCSAGVGRGV 405  
 |||||

Db 1105 PLVHCSAGVGRGV 1119

#### RESULT 5

A57068

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type f - mouse (fragment)

N/Alternate names: leukocyte antigen-related protein LAR

C/Species: Mus musculus (house mouse)

C/Date: 03-Oct-1995 #sequence\_revision 09-Mar-1996 #text\_change 23-Jul-1999

C/Accession: A57068; S40280

R/Schappaveld, R.O.J.; van den Maagdenberg, A.M.J.M.; Schepens, J.T.G.; Olde Weghuis, D.

Genomics 27, 124-130, 1995

A/Title: The mouse gene Pdpf encoding the leukocyte common antigen-related molecule LA

A/Reference number: A57068; MUID:95394448; PMID:765159

A/Accession: A57068

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-582 <SCH>

A/Cross-references: GB:Z37988; NID:G993005; PIDN:CAA66070.1; PID:G993006

R/Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.

submitted to the EMBL Data Library, June 1993

A/Description: Assessment of the expression levels of murine protein-tyrosine phosphatase

A/Reference number: S40280

A/Accession: S40280

A/Molecule type: mRNA

A/Residues: 116-221 <HEN>

A/Cross-references: EMBL:Z23049; NID:G438135; PIDN:CAA80584.1; PID:G438136

C/Genetics:

A/Genetics: Pdpf

C/Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;

C/Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane

F/1-582/Domain: leukocyte common antigen cytosolic domain homology (fragment) <LAC>

F/339-562/Domain: protein-tyrosine-phosphatase homology <PTP2>

F/223/Active site: Cys (phosphocysteine intermediate) #status predicted

F/129/Binding site: substrate phosphate (Arg) #status predicted

F/514/Active site: Cys (phosphocysteine intermediate) #status predicted

F/520/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.0%; Score 14; DB 2; Length 582;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 394 VHCAGVGRGVFI 407  
 |||||

Db 512 VHCAGVGRGVFI 525

#### RESULT 6

S53089

protein-tyrosine-phosphatase (EC 3.1.3.48) Anlar - African malaria mosquito (fragment)

N/Alternate names: leukocyte antigen-related protein

C/Species: Anopheles gambiae (African malaria mosquito)

C/Date: 08-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000

C/Accession: S53089

R/Spiers, S.

submitted to the EMBL Data Library, March 1995

A/Description: Anlar-a transmembrane, receptor-like protein tyrosine phosphatase from tl

A/Reference number: S53089

A/Accession: S53089

A/Molecule type: DNA

A/Residues: 1-1231 <SPI>

A/Cross-references: EMBL:X65217; NID:G732549; PIDN:CAA59483.1; PID:G732550

C/Genetics:

A/Introns: 1026/3; 1070/3; 1209/3

C/Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;

ogy

C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane  
 F:208-293/Domain: fibronectin type III repeat homology <3FR>  
 F:619-1231/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
 F:988-1211/Domain: protein-tyrosine-phosphatase homology <PTP>  
 F:872/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:1163/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:1169/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.0%; Score 14; DB 2; Length 1231;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 394 VHCSAGVGRGVFI 407  
 |||||  
 Db 1161 VHCSAGVGRGVFI 1174

# RESULT 7

A56493

leucocyte common antigen-related protein (LAR) - rat (fragment)

N:Alternate names: LAR receptor-linked tyrosine phosphatase

C:Species: Rattus norvegicus (Norway rat)

C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 21-Jan-2000

C:Accession: A56493; 155393

R:Zhang, J.S.; Longo, F.M.

J. Cell Biol. 128, 415-431, 1995

A:Title: LAR tyrosine phosphatase receptor: alternative splicing is preferential to the

A:Reference number: A56493; PMID:95146548; PMID:7644155

A:Accession: A56493

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1290 <RES>

A:Cross-references: EMBL:X83505; NID:9332918; PIDN:CAA58495.1; PID:9332919

R:Longo, F.M.; Martignetti, J.A.; Le Beau, J.M.; Zhang, J.S.; Barnes, J.P.; Brosius, J.

J. Biol. Chem. 268, 26503-26511, 1993

A:Title: Leukocyte common antigen-related receptor-linked tyrosine phosphatase. Regulation

A:Reference number: 155393; PMID:94073340; PMID:8253779

A:Accession: 155393

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 831-1290 <RES>

A:Cross-references: EMBL:U00477; NID:9392565; PIDN:AAC04306.1; PID:9392566

C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;

Oy

C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase

F:80-166/Domain: fibronectin type III repeat homology <3FR>

F:667-1390/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:1047-1270/Domain: protein-tyrosine-phosphatase homology <PTP2>

F:931/Active site: Cys (phosphocysteine intermediate) #status predicted

F:931/Binding site: substrate phosphate (Arg) #status predicted

F:1222/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1228/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.0%; Score 14; DB 2; Length 1290;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 394 VHCSAGVGRGVFI 407  
 |||||  
 Db 1220 VHCSAGVGRGVFI 1233

# RESULT 8

A48758

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor-linked form PI precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: A48758

R:Pan, M.G.; Rim, C.; Lu, K.P.; Florio, T.; Stock, P.J.S.

J. Biol. Chem. 268, 19284-19291, 1993

A:Title: Cloning and expression of two structurally distinct receptor-linked protein-tyr

A:Reference number: A48758; PMID:93374907; PMID:8396131

A:Accession: A48758

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1496 <PAN>

A:Cross-references: GB:119180

A>Note: authors translated the codon TGC for residue 27 as Gly, GAG for residue 79 as C

as Phe

C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;

Oy

C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; trans

F:149-209/Domain: immunoglobulin homology <IMM1>

F:246-300/Domain: immunoglobulin homology <IMM2>

F:318-405/Domain: fibronectin type III repeat homology <FN3A>

F:411-504/Domain: fibronectin type III repeat homology <FN3B>

F:509-599/Domain: fibronectin type III repeat homology <FN3C>

F:600-684/Domain: fibronectin type III repeat homology <FN3H>

F:880-1496/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:1256-1477/Domain: protein-tyrosine-phosphatase homology <PTP2>

F:1140/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1146/Binding site: substrate phosphate (Arg) #status predicted

F:1429/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1335/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.0%; Score 14; DB 1; Length 1496;  
 Best Local Similarity 100.0%; Pred. No. 2e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 394 VHCSAGVGRGVFI 407  
 |||||  
 Db 1427 VHCSAGVGRGVFI 1440

# RESULT 9

I50212

protein-tyrosine-phosphatase (EC 3.1.3.48) - chicken

C:Species: Gallus gallus (chicken)

C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jan-2000

C:Accession: I50212

R:Stoker, A.W.

Mech. Dev. 46, 201-217, 1994

A:Title: Isoforms of a novel cell adhesion molecule-like protein tyrosine phosphatase a

A:Reference number: I50212; PMID:95001563; PMID:7918104

A:Accession: I50212

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1499 <STO>

A:Cross-references: GB:I32780; NID:9485746; PIDN:AAA64460.1; PID:9485747

C:Genetics:

A:Gene: CRYPalpal

C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;

Oy

C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase

F:148-208/Domain: immunoglobulin homology <IMM1>

F:245-299/Domain: immunoglobulin homology <IMM2>

F:317-399/Domain: fibronectin type III repeat homology <FN3A>

F:881-1499/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:1257-1479/Domain: protein-tyrosine-phosphatase homology <PTP2>

F:1141/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1147/Binding site: substrate phosphate (Arg) #status predicted

F:1432/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1388/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.0%; Score 14; DB 2; Length 1499;  
 Best Local Similarity 100.0%; Pred. No. 2e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 394 VHCSAGVGRGVFI 407  
 |||||  
 Db 1430 VHCSAGVGRGVFI 1443

# RESULT 10

I38148

protein-tyrosine-phosphatase (EC 3.1.3.48) 2B, splice form IAR - rat  
 N:Alternate names: leukocyte common antigen-related phosphatase  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 20-Jun-2000  
 C:Accession: 158148, S46218  
 R:Malton, K.M.; Martell, K.J.; Kwak, S.P.; Dixon, J.E.; Largent, B.L.  
 R:Neuron 11, 387-400, 1993  
 A:Title: A novel receptor-type protein tyrosine phosphatase is expressed during neurogen  
 A:Reference number: 158148, MUID:93357030, PMID:8352946  
 A:Accession: 158148  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1501 <NAL>  
 A:Cross-references: GB:LI9933; NID:G310242; PIDN:AAA42309.1; PID:G310243  
 A>Note: in Genbank entry RATTYRPHOS, release 113.0, the source is designated as Rattus r  
 R:Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.  
 Biochem. J. 302, 39-47, 1994  
 A:Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-ph  
 A:Reference number: S46216, MUID:94347119, PMID:8068021  
 A:Accession: S46218  
 A:Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-1501 <ZHA>  
 A:Cross-references: EMBL:LI2329; NID:G294573; PIDN:AA37657.1; PID:G294574  
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
 C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolyase; tyrosi  
 Cgy  
 F:47-109/Domain: immunoglobulin homology <IMM1>  
 F:149-209/Domain: immunoglobulin homology <IMW2>  
 F:246-300/Domain: immunoglobulin homology <IMW3>  
 F:411-506/Domain: fibronectin type III repeat homology <FTR>  
 F:882-1501/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
 F:969-1190/Domain: protein-tyrosine-phosphatase homology <PTR>  
 F:1258-1481/Domain: protein-tyrosine-phosphatase homology <PTR2>  
 F:1142/Active site: Cys (phosphocysteine intermediate) #link PTP #status predicted  
 F:118/Binding site: substrate phosphate (Arg) #link PTP #status predicted  
 F:143/Active site: Cys (phosphocysteine intermediate) #link PTP #status predicted  
 F:143/Binding site: substrate phosphate (Arg) #link PTP #status predicted

Query Match 3.0%; Score 14; DB 2; Length 1501;  
 Best Local Similarity 100.0%; Pred. No. 2e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 394 VHCSAGVGRGVFI 407  
 Db 1431 VHCSAGVGRGVFI 1444

RESULT 11

D54689  
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form D precursor  
 N:Alternate names: MPPR delta type D  
 N:Contains: protein tyrosine phosphatase, receptor type delta, splice form A  
 C:Species: Mus musculus (house mouse)  
 C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: D54689, A54669  
 R:Mizuno, K.; Hasegawa, K.; Katsigiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.  
 M:Cell. Biol. 13, 5513-5523, 1993  
 A:Title: MPPR delta, a putative murine homolog of HPPR delta, is expressed in specializ  
 A:Reference number: A54689, MUID:93360986, PMID:8355697  
 A:Accession: D54689  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1691 <MT>  
 A:Experimental source: brain  
 A>Note: sequence inconsistent with nucleotide translation  
 A:Accession: A54689  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1398, 799-1691 <MT2>  
 A:Experimental source: brain  
 A>Note: sequence inconsistent with nucleotide translation

A>Note: sequence extracted from NCBI backbone (NCBIN:136522, NCBI:136524)  
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
 Cgy  
 C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hy  
 F:42-99/Domain: immunoglobulin homology <IMW3>  
 F:114-196/Domain: fibronectin type III repeat homology <FNA>  
 F:1075-1691/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
 F:1449-1671/Domain: protein-tyrosine-phosphatase homology <PTR>  
 F:1333/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:1339/Binding site: substrate phosphate (Arg) #status predicted  
 F:1623/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:1629/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.0%; Score 14; DB 1; Length 1691;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 394 VHCSAGVGRGVFI 407  
 Db 1621 VHCSAGVGRGVFI 1634

RESULT 12

S46217  
 protein-tyrosine-phosphatase (EC 3.1.3.48) type sigma precursor - rat  
 N:Alternate names: leukocyte common antigen-related phosphatase  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 07-May-1995 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999  
 C:Accession: S46217, S51174, A49104  
 R:Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.  
 Biochem. J. 302, 39-47, 1994  
 A:Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-ph  
 A:Reference number: S46216, MUID:94347119, PMID:8068021  
 A:Accession: S46217  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-1863 <ZHA>  
 A:Cross-references: EMBL:LI1587  
 R:Goldstein, B.J.  
 submitted to the EMBL Data Library, February 1993  
 A:Reference number: S51174  
 A:Accession: S51174  
 A:Molecule type: mRNA  
 A:Residues: 1-1788, 'G', 1790-1863 <GOL>  
 A:Cross-references: EMBL:LI1587; NID:G205134; PIDN:AA37656.1; PID:G205135  
 R:Yan, H.; Grossman, A.; Wang, H.; D'Esposito, P.; Mossie, K.; Musacchio, J.M.; Silvan  
 J. Biol. Chem. 268, 24880-24886, 1993  
 A:Title: A novel receptor tyrosine phosphatase-sigma that is highly expressed in the ne  
 A:Reference number: A49104, MUID:94043351, PMID:8227050  
 A:Accession: A49104  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: nucleic acid  
 A:Residues: 1-596, 'R', 598-603, 'I', 967-1788, 'G', 1790-1863 <YAN>  
 A:Experimental source: brain  
 A>Note: sequence extracted from NCBI backbone (NCBI:139669)  
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
 Cgy  
 C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hy  
 F:1-56/Domain: signal sequence #status predicted <SIG>  
 F:217-1863/Domain: protein-tyrosine-phosphatase #status predicted <WAT>  
 F:148-209/Domain: immunoglobulin homology <IMW2>  
 F:246-300/Domain: immunoglobulin homology <IMW3>  
 F:318-400/Domain: fibronectin type III repeat homology <FNA>  
 F:413-499/Domain: fibronectin type III repeat homology <FNA3>  
 F:511-592/Domain: fibronectin type III repeat homology <FNA3>  
 F:1244-1863/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
 F:1131-1552/Domain: protein-tyrosine-phosphatase homology <PTR>  
 F:1504/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:1504/Binding site: substrate phosphate (Arg) #status predicted  
 F:1795/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:1801/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.0%; Score 14; DB 2; Length 1863;

Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 394 VHCAGVGRGTGVPF 407  
|||||

Db 1793 VHCAGVGRGTGVPF 1806

# RESULT 13

C54689  
protein-tyrosine-phosphatase (BC 3.1.3.48), receptor type delta, splice form B precursor  
N:Alternate names: MPTP delta type B/C  
N:Contains: protein tyrosine phosphatase, receptor type delta, splice form C  
C:Species: Mus musculus (house mouse)  
C>Date: 25-Apr-1995 #sequence\_revision 19-May-1995 #text\_change 12-Feb-1999  
C:Accession: C54689; B54689  
R:Matsumoto, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.  
Mol. Cell. Biol. 13, 5513-5523, 1993  
A:Title: MPTP delta, a putative murine homolog of HPTP delta, is expressed in specialized  
A:Reference number: A54689; MUID:93360986; PMID:8355697  
A:Accession: C54689  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1894 <M12>  
A:Experimental source: Brain; splice form B  
A:Note: sequence inconsistent with nucleotide translation  
A:Note: sequence extracted from NCBI backbone (NCBIN:137486, NCBI:137487)  
A:Accession: B54689  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-352, 'H', 354-535, 'S', 537-601, 1002-1894 <M12>  
A:Experimental source: Brain; splice form C  
A:Note: sequence inconsistent with nucleotide translation  
A:Note: sequence extracted from NCBI backbone (NCBIN:136527, NCBI:136530)  
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
QY  
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd  
F:45-107/Domain: immunoglobulin homology <IM1>  
F:245-299/Domain: immunoglobulin homology <IM2>  
F:317-399/Domain: fibronectin type III repeat homology <FN3A>  
F:1278-1894/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F:1652-1874/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F:1542/Binding site: Cys (phosphocysteine intermediate) #status predicted  
F:1542/Active site: substrate phosphate (Arg) #status predicted  
F:1826/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1832/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.0%; Score 14; DB 2; Length 1894;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 394 VHCAGVGRGTGVPF 407  
|||||

Db 1824 VHCAGVGRGTGVPF 1837

# RESULT 14

TDRULK  
leukocyte antigen-related protein precursor - human  
N:Alternate names: leukocyte common antigen homology  
N:Contains: protein-tyrosine-phosphatase (BC 3.1.3.48)  
C:Species: Homo sapiens (man)  
C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 22-Jun-1999  
C:Accession: S03841; J10051  
R:Streuli, M.; Krueger, N.X.; Hall, L.R.; Schlossman, S.F.; Saito, H.  
J. Exp. Med. 168, 1523-1530, 1988  
A:Title: A new member of the immunoglobulin superfamily that has a cytoplasmic region ho  
A:Reference number: J10051; MUID:89035978; PMID:2972192  
A:Accession: S03841  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-1897 <STR>  
A:Cross-references: EMBL:Y00815; NID:G34266; P1DN:CAA68754.1; P1D:G34267

C:Genetics: LAR

A:Cross-references: GDB:120138; OMIM:179590

A:Map position: 1P34-1P34

C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
QY

C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:17-1897/Product: leukocyte antigen-related protein #status predicted <MAT>  
F:17-1250/Domain: extracellular #status predicted <EXT>  
F:33-99/Domain: immunoglobulin homology <IM1>  
F:219-199/Domain: immunoglobulin homology <IM2>  
F:226-290/Domain: immunoglobulin homology <IM3>  
F:308-390/Domain: fibronectin type III repeat homology <FN3A>  
F:403-489/Domain: fibronectin type III repeat homology <FN3B>  
F:501-583/Domain: fibronectin type III repeat homology <FN3C>  
F:586-685/Domain: fibronectin type III repeat homology <FN3D>  
F:698-798/Domain: fibronectin type III repeat homology <FN3E>  
F:810-893/Domain: fibronectin type III repeat homology <FN3F>  
F:905-989/Domain: fibronectin type III repeat homology <FN3G>  
F:1001-1078/Domain: fibronectin type III repeat homology <FN3H>  
F:1251-1274/Domain: transmembrane #status predicted <TM>  
F:1275-1897/Domain: intracellular #status predicted <INT>  
F:1285-1897/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F:1365-1586/Domain: protein-tyrosine-phosphatase homology <PTP1>  
F:1654-1877/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F:44-97, 146-197, 243-288/Disulfide bonds: #status predicted  
F:107-240, 285, 711, 956/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:1538/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1544/Binding site: substrate phosphate (Arg) #status predicted  
F:1829/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1835/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.0%; Score 14; DB 1; Length 1897;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 394 VHCAGVGRGTGVPF 407  
|||||

Db 1827 VHCAGVGRGTGVPF 1840

# RESULT 15

S46216  
leukocyte antigen-related protein precursor - rat  
N:Alternate names: leukocyte common antigen homology  
N:Contains: protein-tyrosine-phosphatase (BC 3.1.3.48)  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C:Accession: S46216; S23252; A41032; A33154  
R:Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.  
Biochem. J. 302, 39-47, 1994  
A:Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-ph  
A:Reference number: S46216; MUID:94347119; PMID:8068021  
A:Accession: S46216  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-1898 <ZHA>  
A:Cross-references: EMBL:L11586; NID:G205132; P1DN:AA037655.1; P1D:G205133  
R:Hashimoto, N.; Zhang, W.R.; Goldstein, B.J.  
Biochem. J. 284, 569-576, 1992  
A:Title: Insulin receptor and epidermal growth factor receptor dephosphorylation by thr  
A:Reference number: S23252; MUID:92287069; PMID:1559438  
A:Accession: S23252  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1361-1604, 1649-1898 <HAS>  
R:Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.  
J. Biol. Chem. 266, 19688-19696, 1991  
A:Title: Cloning, bacterial expression, purification, and characterization of the cytop  
A:Reference number: A41032; MUID:92011772; PMID:1918076  
A:Accession: A41032  
A:Molecule type: mRNA

A:Residues: 1035-1072, 'S', 1074-1433, 'T', 1435-1638, 'N', 1640-1642, 'HT', 1645-1898 <POT>  
 A:Cross-references: GB:M60103; NID:G205130; PID:AAA41510.1; PID:G205131  
 R:Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.  
 Submitted to the Protein Sequence Database, December 1990  
 A:Reference number: A33154  
 A:Accession: A33154  
 A:Molecule type: mRNA  
 C:Residues: 1035-1072, 'S', 1074-1433, 'T', 1435-1638, 'N', 1640-1642, 'HT', 1645-1898 <PO2>  
 C:Comment: Only the first of the two domains homologous with protein-tyrosine-phosphatase  
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
 OGY  
 C:Keywords: duplication; glycoprotein; phosphoprotein; phosphoric monoester hydrolase; t  
 F:1-27/Domain: (or 1-26) signal sequence #status predicted <SIG>  
 F:28-1898/Product: (or 27-1898) leukocyte antigen-related protein #status predicted <MAT  
 F:28-1251/Domain: (or 27-1251) extracellular #status predicted <EXT>  
 F:47-109/Domain: immunoglobulin homology <IMM1>  
 F:149-209/Domain: immunoglobulin homology <IMM2>  
 F:246-300/Domain: immunoglobulin homology <IMM3>  
 F:318-400/Domain: fibronectin type III repeat homology <FN3A>  
 F:413-499/Domain: fibronectin type III repeat homology <FN3B>  
 F:511-593/Domain: fibronectin type III repeat homology <FN3C>  
 F:606-695/Domain: fibronectin type III repeat homology <FN3D>  
 F:708-799/Domain: fibronectin type III repeat homology <FN3E>  
 F:811-895/Domain: fibronectin type III repeat homology <FN3F>  
 F:906-990/Domain: fibronectin type III repeat homology <FN3G>  
 F:1002-1078/Domain: fibronectin type III repeat homology <FN3H>  
 F:1252-1275/Domain: (or 1259-1275) transmembrane #status predicted <TM>  
 F:1276-1898/Domain: intracellular #status predicted <INT>  
 F:1286-1898/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
 F:1366-1587/Domain: protein-tyrosine-phosphatase homology <PTP1>  
 F:1655-1878/Domain: protein-tyrosine-phosphatase homology <PTP2>  
 F:54-107,156-207,253-298/Diulfide bonds:#status predicted  
 F:117,250,295,721,957/Binding site: carbohydrate (asn) (covalent) #status predicted  
 F:1539/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:1545/Binding site: substrate phosphate (Arg) #status predicted  
 F:1830/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:1836/Binding site: substrate phosphate (Arg) #status predicted  
 Query Match 3.0%; Score 14; DB 2; length 1898;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 394 VHCAGVGRITGVFI 407  
 DB 1828 VHCAGVGRITGVFI 1841  
 Search completed: June 18, 2004, 19:49:16  
 Job time : 22 secs



GenCore version 5.1.6  
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OW protein - protein search, using sw model

Run on: June 18, 2004, 19:41:14 ; Search time 17 Seconds

(without alignments)  
1418.146 Million cell updates/sec

Title: US-09-095-478A-6

Perfect score: 463  
Sequence: 1 MSSPRKRYKRTGRDNDEEG.....QYQFCYETLVENQLNLLAL 463

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size: 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	3.2	1174	1	PTNL_HUMAN
2	15	3.2	1175	1	PTNL_RAT
3	15	3.2	1176	1	PTNL_MOUSE
4	14	3.0	1897	1	PTPF_HUMAN
5	14	3.0	1912	1	PTPD_HUMAN
6	14	3.0	1948	1	PTNS_HUMAN
7	12	2.6	1187	1	PTNE_HUMAN
8	12	2.6	1189	1	PTNE_MOUSE
9	12	2.6	1238	1	PTPJ_MOUSE
10	12	2.6	1337	1	PTPJ_HUMAN
11	12	2.6	1442	1	PTPG_MOUSE
12	12	2.6	1445	1	PTPG_HUMAN
13	12	2.6	1462	1	PTPV_MOUSE
14	12	2.6	1705	1	PTPV_MOUSE
15	12	2.6	1711	1	PTPV_RAT
16	11	2.4	325	1	PTPI_YEAST
17	11	2.4	531	1	PTPI_DICDI
18	11	2.4	550	1	PTPI_SCHPO
19	11	2.4	699	1	PTPE_MOUSE
20	11	2.4	700	1	PTPE_HUMAN
21	11	2.4	711	1	PTP2_SCHPO
22	11	2.4	766	1	PTPA_RAT
23	11	2.4	802	1	PTPA_HUMAN
24	11	2.4	829	1	PTPA_MOUSE
25	11	2.4	1152	1	CD45_MOUSE
26	11	2.4	1216	1	CD45_HUMAN
27	11	2.4	1255	1	CD45_RAT
28	11	2.4	1301	1	PTP9_DROME
29	11	2.4	1304	1	CD45_HUMAN
30	11	2.4	1422	1	PTPG_CHICK
31	11	2.4	1977	1	PTPB_HUMAN
32	11	2.4	2029	1	PTPB_MOUSE
33	11	2.4	2200	1	LAR_CAEEL

34	11	2.4	2314	1	PTP2_HUMAN	P23471 homo sapien
35	11	2.4	2316	1	PTP2_RAT	Q62656 rattus norv
36	9	1.9	458	1	PTNI_HUMAN	Q99952 homo sapien
37	9	1.9	750	1	PTP2_YEAST	P29461 saccharomyc
38	9	1.9	913	1	PTN3_HUMAN	P26045 homo sapien
39	9	1.9	1001	1	PTPX_MOUSE	P80560 mus musculu
40	9	1.9	1004	1	PTPX_RAT	Q63475 rattus norv
41	9	1.9	1013	1	PTPX_MACNE	Q02695 macaca neme
42	9	1.9	1015	1	PTPX_HUMAN	Q92932 homo sapien
43	9	1.9	1631	1	PTPI_DROME	P35992 dirosophila
44	8	1.7	117	1	PT25_STYPL	P28217 styela pilic
45	8	1.7	573	1	C114_MOUSE	P19467 mus musculu

## ALIGNMENTS

```

RESULT 1
PTNL_HUMAN          STANDARD;          PRT; 1174 AA.
ID
AC Q16825;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 21 (EC 3.1.3.48)
DE (Protein-tyrosine phosphatase D1).
GN PTPN21 OR PTPD1.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stkeletal muscle;
RX MEDLINE=94329538; PubMed=7519780;
RA Koeller N.P.H., Koeller K.B., Lammers R., Kharronenkov A., Sures I.,
RA Ullrich A.;
RT "Src kinase associates with a member of a distinct subfamily of
RT protein-tyrosine phosphatases containing an ezrin-like domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:7477-7481(1994).
CC -|- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H2O = protein
CC tyrosine + phosphate.
CC -|- SIMILARITY: Contains 1 PFM domain.
CC -|- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X79510; CA56042.1; -
DR PIR: I38140; I38140.
DR HSSP: Q06124; ZSHP.
DR Genew: HGNC:9651; PTPN21.
DR KIM: 603271; -
DR GO: GO:0005856; C:cytoskeleton; TAS.
DR GO: GO:0004725; F:protein tyrosine phosphatase activity; TAS.
DR GO: GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR InterPro: IPR000299; Band 4.1.
DR InterPro: IPR000387; Tyr_P.
DR InterPro: IPR000242; Tyr_PP.
DR Pfam: PF00373; Band 41; 1.
DR Pfam: PF00102; Y phosphatase; 1.
DR PRINTS: PR00935; BAND41.
DR PRINTS: PR00700; PTPYHPHTASE.
DR SMART: SM00295; B41; 1.
DR SMART: SM00194; PTPC; 1.
DR PROSITE: PS00660; FERM_1; 1.
DR PROSITE: PS00661; FERM_2; 1.

```

DR PROSITE; PS50057; FERM\_3; 1.  
 DR PROSITE; PS50083; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 1.  
 DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 1.  
 KW Structural protein; Cytoskeleton; Hydrolase.  
 FT DOMAIN 23 308 FERM.  
 FT ACT\_SITE 1108 1108 PROTEIN-TYROSINE PHOSPHATASE.  
 FT ACT\_SITE 1108 1108 PHOSPHOCYSTEINE INTERMEDIATE  
 (BY SIMILARITY).  
 FT DOMAIN 340 343 POLY-PRO.  
 FT DOMAIN 515 517 POLY-PRO.  
 FT DOMAIN 712 714 POLY-GU.  
 SQ SEQUENCE 1174 AA; 133287 MW; 57729B1A93B3FDA CRC64;  
 Query Match 3.2%; Score 15; DB 1; Length 1174;  
 Best Local Similarity 100.0%; Pred. No. 4e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 391 PLVHCSAGVGRGV 405  
 DB 1103 PLVHCSAGVGRGV 1117

RESULT 2  
 PTNL\_RAT STANDARD; PRT; 1175 AA.

AC Q62728; Q62732; (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein tyrosine phosphatase, non-receptor type 21 (EC 3.1.3.48)  
 DE (Protein-tyrosine phosphatase 2E).  
 GN PTPN21 OR PTP2E.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_Taxid=10116;  
 [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2E).  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=9510449; PubMed=7805871;  
 RA L'Abbe D., Banville D., Tong Y., Stocco R., Masson S., Ma S.,  
 RA Fatus G., Shen S.H.;  
 RA Identification of a novel protein tyrosine phosphatase with sequence  
 RT homology to the cytoskeletal proteins of the band 4.1 family.";  
 RL FEBS Lett. 356:351-356(1994).  
 CC -1 CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -1 ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=Q62728-1; Sequence=Displayed;  
 CC Name=2E;  
 CC IsoId=Q62728-2; Sequence=VSP\_000498;  
 CC -1 TISSUE SPECIFICITY: Particularly abundantly in adrenal glands.  
 CC -1 SIMILARITY: Contains 1 FERM domain.  
 CC -1 SIMILARITY: Belongs to the protein-tyrosine phosphatase family.  
 CC Non-receptor class subfamily.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; U17971; AA62153.1; -  
 CC EMBL; U18293; AA62154.1; -  
 CC PIR; S51005; S51005.  
 CC HSSP; Q06124; 2SHF.  
 CC InterPro; IPR000299; Band 4.1.  
 CC InterPro; IPR000387; TYR\_phosphatase.

DR InterPro; IPR000242; Tyr\_PP.  
 DR Pfam; PF00373; Band 41; 1.  
 DR Pfam; PF00102; Y-phosphatase; 1.  
 DR PRINTS; PR00935; BAND41.  
 DR PRINTS; PR00700; PRTYPHTASE.  
 DR SMART; SM00295; P41; 1.  
 DR SMART; SM00194; PTPC; 1.  
 DR PROSITE; PS00660; FERM\_1; 1.  
 DR PROSITE; PS00661; FERM\_2; 1.  
 DR PROSITE; PS50057; FERM\_3; 1.  
 DR PROSITE; PS50058; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 1.  
 DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 1.  
 KW Structural protein; Cytoskeleton; Hydrolase; Alternative splicing.  
 FT DOMAIN 23 308 FERM.  
 FT DOMAIN 922 1175 PROTEIN-TYROSINE PHOSPHATASE.  
 FT ACT\_SITE 1109 1109 PHOSPHOCYSTEINE INTERMEDIATE  
 (BY SIMILARITY).  
 FT VARSPLIC 1 839 Missing (in isoform 2E).  
 FT  
 SQ SEQUENCE 1175 AA; 133411 MW; 82A684F1C0F5ECF7 CRC64;  
 Query Match 3.2%; Score 15; DB 1; Length 1175;  
 Best Local Similarity 100.0%; Pred. No. 4e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 391 PLVHCSAGVGRGV 405  
 DB 1104 PLVHCSAGVGRGV 1118

RESULT 3  
 PTNL\_MOUSE STANDARD; PRT; 1176 AA.

AC Q62136;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein tyrosine phosphatase, non-receptor type 21 (EC 3.1.3.48)  
 DE (Protein-tyrosine phosphatase PTP-RL10).  
 GN PTPN21.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_Taxid=10090;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Liver;  
 RX MEDLINE=9510431; PubMed=7838537;  
 RA Higaahitsuji H., Arai S., Furutani M., Imamura M., Kaneko Y.,  
 RA Takemura J., Nakayama H., Fujita J.;  
 RA Enhanced expression of multiple protein tyrosine phosphatases in the  
 RT regenerating mouse liver: isolation of PTP-RL10, a novel cytoplasmic-  
 RT type phosphatase with sequence homology to cytoskeletal protein  
 RT 4.1.";  
 RL Oncogene 10:407-414(1995).  
 CC -1 FUNCTION: May be involved in the regulation of growth and  
 CC differentiation of liver cells.  
 CC -1 CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -1 TISSUE SPECIFICITY: Liver.  
 CC -1 SIMILARITY: Contains 1 FERM domain.  
 CC -1 SIMILARITY: Belongs to the protein-tyrosine phosphatase family.  
 CC Non-receptor class subfamily.  
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DR EMBL: D37801; BAA07053.1; -  
 DR PIR: I58345; I58345.  
 DR HSSP: P29350; IGM2.  
 DR MGD: MGI:1344406; Pgn21.  
 DR InterPro: IPR000299; Band 4.1.  
 DR InterPro: IPR000387; TYR Phosphatase.  
 DR InterPro: IPR000242; Tyr DP.  
 DR Pfam: PF00373; Band 41; I.  
 DR Pfam: PF00102; Y\_phosphatase; 1.  
 DR PRINTS: PR00935; BAND41.  
 DR PRINTS: PR00700; PRTYPHPTASE.  
 DR SMART: SM00295; B41; 1.  
 DR SMART: SM00134; PTPc; 1.  
 DR PROSITE: PS00660; FERM 1; 1.  
 DR PROSITE: PS00661; FERM 2; 1.  
 DR PROSITE: PS00557; FERM 3; 1.  
 DR PROSITE: PS00383; TYR PHOSPHATASE 1; 1.  
 DR PROSITE: PS00055; TYR PHOSPHATASE PTP; 1.  
 DR PROSITE: PS00056; TYR PHOSPHATASE 2; 1.  
 DR Structural protein; Cytoskeleton; Hydrolase.  
 KW DOMAIN 23 308 FERM  
 FT DOMAIN 923 1176 PROTEIN-TYROSINE PHOSPHATASE.  
 FT ACT\_SITE 1110 1110 PHOSPHOCYSTEINE INTERMEDIATE  
 (BY SIMILARITY).  
 FT DOMAIN 340 343 POLY-PRO.  
 FT DOMAIN 565 572 POLY-PRO.  
 SQ SEQUENCE 1176 AA; 133490 MW; 529FBE22F1335B75 CRC64;

Query Match 3.2%; Score 15; DB 1; Length 1176;  
 Best Local Similarity 100.0%; Pred. No. 4e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 391 PLVHCSAGVGRGV 405  
 Db 1105 PLVHCSAGVGRGV 1119

RESULT 4  
 PTPF\_HUMAN STANDARD; PRT; 1897 AA.  
 AC P10586;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE IAR protein precursor (leukocyte antigen related) (EC 3.1.3.48).  
 GN PTPRF OR IAR.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 CC NCBI\_taxid=9606;  
 OK NCBI [1]  
 RN RP SEQUENCE FROM N.A.  
 RN RC TISSUE=Toes1;  
 RX MEDLINE=89035978; PubMed=2972792;  
 RA Streuli M., Krueger N.X., Hall L.R., Schlossman S.F., Saito H.;  
 RT "A new member of the immunoglobulin superfamily that has a  
 RT cytoplasmic region homologous to the leukocyte common antigen";  
 RL J. Exp. Med. 168:1523-1530(1988).  
 RN RN [2]  
 RN RP MUTAGENESIS.  
 RX MEDLINE=90046860; PubMed=2554325;  
 RA Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;  
 RT "A family of receptor-linked protein tyrosine phosphatases in humans  
 RT and Drosophila";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).  
 RN RN [3]  
 RN RP MUTAGENESIS.  
 RX MEDLINE=90316093; PubMed=1695146;  
 RA Streuli M., Krueger N.X., Thai T., Tang M., Saito H.;  
 RT "Distinct functional roles of the two intracellular phosphatase like  
 RT domains of the receptor-linked protein tyrosine phosphatases LCA and  
 RT IAR";  
 RL EMBO J. 9:2399-2407(1990).

CC -1- FUNCTION: It is possible that IAR is a cell adhesion receptor.  
 CC It possesses an intrinsic protein tyrosine phosphatase activity  
 CC (PTPase).  
 CC -1- FUNCTION: The first PTPase domain has enzymatic activity, while  
 CC the second one seems to affect the substrate specificity of the  
 CC first one.  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.  
 CC -1- SIMILARITY: Contains 8 fibronectin type III domains.  
 CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
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 CC -----  
 DR EMBL: Y00815; CA68754.1; -  
 DR PIR: S03841; THYUK.  
 DR PDB: IAR; 25-APR-00.  
 DR Genew; HGNC:9670; PTPRF.  
 DR KIM; 179590; -  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. . .; TAS.  
 DR GO; GO:0007155; P:cell adhesion; TAS.  
 DR GO; GO:0007485; P:transmembrane receptor protein tyrosine pho. . .; TAS.  
 DR InterPro: IPR008957; FN\_III-like.  
 DR InterPro: IPR003961; FN\_III.  
 DR InterPro: IPR003962; FNIII subd.  
 DR InterPro: IPR007110; Ig\_1-like.  
 DR InterPro: IPR003598; Ig\_C2.  
 DR InterPro: IPR000387; TYR phosphatase.  
 DR InterPro: IPR000242; Tyr\_PP.  
 DR Pfam; PF00041; Fn3; 7.  
 DR Pfam; PF00047; Ig; 3.  
 DR Pfam; PF00102; Y\_phosphatase; 2.  
 DR PRINTS: PR00014; FMYPEPIL.  
 DR PRINTS: PR00700; PRTYPHPTASE.  
 DR SMART; SM00060; FN3; 4.  
 DR SMART; SM00408; IGC2; 3.  
 DR SMART; SM00194; PTPc; 2.  
 DR PROSITE; PS50835; IG\_LIKE; 3.  
 DR PROSITE; PS00383; TYR PHOSPHATASE 1; 2.  
 DR PROSITE; PS50056; TYR PHOSPHATASE 2; 2.  
 DR PROSITE; PS50055; TYR PHOSPHATASE\_PTP; 2.  
 DR HydroLase; Receptor; Glycoprotein; Signal; Transmembrane;  
 DR Cell adhesion; Immunoglobulin domain; Repeat; 3D-structure.  
 KW SIGNAL 1 16  
 FT CHAIN 17 1897 LAR PROTEIN.  
 FT DOMAIN 17 1250 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1251 1274 POTENTIAL.  
 FT CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 1275 1897 IG-LIKE C2-TYPE 1.  
 FT DOMAIN 125 113 IG-LIKE C2-TYPE 2.  
 FT DOMAIN 125 214 IG-LIKE C2-TYPE 3.  
 FT DOMAIN 222 304 IG-LIKE C2-TYPE 3.  
 FT DOMAIN 1360 1606 PROTEIN-TYROSINE PHOSPHATASE 1.  
 FT DOMAIN 1649 1897 PROTEIN-TYROSINE PHOSPHATASE 2.  
 FT ACT\_SITE 1538 1538 PHOSPHOCYSTEINE INTERMEDIATE (BY  
 FT SIMILARITY).  
 FT ACT\_SITE 1829 1829 PHOSPHOCYSTEINE INTERMEDIATE (BY  
 FT SIMILARITY).  
 FT CARBOHYD 107 107 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 711 711 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 956 956 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT MUTAGEN 1538 1538 C-S; LOSS OF ACTIVITY  
 SQ SEQUENCE 1897 AA; 211844 MW; 439850FID5C031FF CRC64;

Query Match 3.0%; Score 14; DB 1; Length 1897;  
 Best Local Similarity 100.0%; Pred. No. 7, 1e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 394 VHCAGVGRGVFI 407  
 Db 1827 VHCAGVGRGVFI 1840

RESULT 5  
 PTPD\_HUMAN STANDARD; PRT; 1912 AA.  
 ID PTPD\_HUMAN  
 AC P23468;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein-tyrosine phosphatase delta precursor (EC 3.1.3.48) (R-PTP-delta).  
 GN PTPRD.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1] SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-1178.  
 RP MEDLINE=95204468; PubMed=7896816;  
 RA Pulido R., Krueger N.X., Serra-Pages C., Saito H., Streuli M.;  
 RT "Molecular characterization of the human transmembrane protein-tyrosine phosphatase delta. Evidence for tissue-specific expression of alternative human transmembrane protein-tyrosine phosphatase delta isoforms.";  
 RT J. Biol. Chem. 270:6722-6728 (1995).  
 RL [2]  
 RN RP  
 RP SEQUENCE OF 390-1912 FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=91006018; PubMed=2170109;  
 RA Krueger N.X., Streuli M., Saito H.;  
 RT "Structural diversity and evolution of human receptor-like protein tyrosine phosphatases.";  
 RT EMBO J. 9:3241-3252 (1990).  
 RL  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=3;  
 CC Comment=Additional isoforms seem to exist;  
 CC Name=1;  
 CC IsoId=P23468-1; Sequence=Displayed;  
 CC Name=2; Synonyms=K1dneey;  
 CC IsoId=P23468-2; Sequence=VSP\_005147, VSP\_005148, VSP\_005149;  
 CC Name=3; Synonyms=Fetal brain;  
 CC IsoId=P23468-3; Sequence=VSP\_005150;  
 CC -1- FROM THE TRANSMEMBRANE SEGMENT.  
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.  
 CC -1- SIMILARITY: Contains 8 fibronectin type III domains.  
 CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
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 CC  
 DR EMBL, L38929; AAC1749.1; -;  
 DR EMBL, X54133; CAA38058.1; -;  
 DR PIR, A56178; A56178.  
 DR HSSP, P18052; LYPO.  
 DR Genew; HGNC:9668; PTPRD.  
 DR MIM, 601598; -;  
 DR GO; GO:0005087; C:integral to plasma membrane; TAS.

DR GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. . . ; TAS.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.  
 DR GO; GO:0007185; P:transmembrane receptor protein tyrosine pho. . . ; TAS.  
 DR InterPro; IPR008957; FN\_III-like.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR003962; FNIII\_subd.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003598; Ig\_C2.  
 DR InterPro; IPR000387; Tyr\_phosphatase.  
 DR InterPro; IPR000242; Tyr\_PP.  
 DR Pfam; PF00041; fn3; 8.  
 DR Pfam; PF00047; Ig\_3.  
 DR Pfam; PF00102; Y\_phosphatase; 2.  
 DR PRINTS; PR00014; FNYPHIII.  
 DR PRINTS; PR00700; PRTYPHPTASE.  
 DR SMART; SM00060; FN3; 8.  
 DR SMART; SM00408; IGC2; 2.  
 DR SMART; SM00194; PTPC; 2.  
 DR PROSITE; PS50835; IG\_LIKE; 3.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 2.  
 DR Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane; Repeat; KW Immunoglobulin domain; Alternative splicing.  
 FT SIGNAL 1 20  
 FT CHAIN 21 1912  
 FT DOMAIN 21 1265  
 FT TRANSMEM 1266 1290  
 FT DOMAIN 1291 1912  
 FT DOMAIN 24 114  
 FT DOMAIN 126 224  
 FT DOMAIN 236 318  
 FT DOMAIN 320 414  
 FT DOMAIN 417 513  
 FT DOMAIN 516 606  
 FT DOMAIN 609 708  
 FT DOMAIN 711 822  
 FT DOMAIN 825 916  
 FT DOMAIN 918 1017  
 FT DOMAIN 1020 1618  
 FT DOMAIN 1375 1618  
 FT DOMAIN 1619 1912  
 FT ACT\_SITE 1553 1553  
 FT ACT\_SITE 1844 1844  
 FT SITE 1175 1178  
 FT CARBOHYD 254 254  
 FT CARBOHYD 299 299  
 FT CARBOHYD 724 724  
 FT CARBOHYD 832 832  
 FT VARSPIC 181 189  
 FT VARSPIC 226 229  
 FT VARSPIC 775 783  
 FT VARSPIC 609 1137  
 FT MUTAGEN 1178 1178  
 FT SEQUENCE 1912 AA; 214759 MW; 3AB8CB032182E26 CRC64;  
 Query Match 3.0%; Score 14; DB 1; Length 1912;  
 Best Local Similarity 100.0%; Pred. No. 7, 2e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 394 VHCAGVGRGVFI 407  
 Db 1842 VHCAGVGRGVFI 1855  
 RESULT 6  
 PTPD\_HUMAN



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FT VARSPLIC 617 1034 Missing (in isoform PTPS-F4-7).
FT VARSPLIC 784 792 /FTId=VSP_050023.
FT VARSPLIC 1035 1035 Missing (in isoform PTPS-MEC).
FT VARSPLIC 1035 1035 /FTId=VSP_050024.
FT VARSPLIC 1350 1365 V->I (in isoform PTPS-F4-7).
FT VARSPLIC 1350 1365 /FTId=VSP_050025.
FT VARSPLIC 1366 1366 Missing (in isoform PTPS-MEB).
FT VARSPLIC 1366 1366 /FTId=VSP_050026.
FT VARSPLIC 1366 1366 S->G (in isoform PTPS-MEB).
FT VARSPLIC 1366 1366 /FTId=VSP_050027.
FT VARSPLIC 1366 1366 T->HP (IN REF. 2).
FT VARSPLIC 1366 1366 SA->RP (IN REF. 2).
FT VARSPLIC 1366 1366 LGPV->RSP (IN REF. 2).
FT VARSPLIC 1366 1366 GAEGRPPR->RREAGRRS (IN REF. 2).
FT VARSPLIC 1366 1366 R->P (IN REF. 2).
FT VARSPLIC 1366 1366 AAEPAENAV->GRLSRRRTL (IN REF. 2).
FT VARSPLIC 1366 1366 TV->SL (IN REF. 2).
FT VARSPLIC 1366 1366 F->S (IN REF. 2).
FT VARSPLIC 1366 1366 E->D (IN REF. 4).
FT VARSPLIC 1366 1366 V->A (IN REF. 4).
FT VARSPLIC 1366 1366 N->K (IN REF. 2).
SQ SEQUENCE 1948 AA; 217080 MW; 7DC049EC03171136 CRC64;

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Query Match 3.0%; Score 14; DB 1; Length 1948;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 394 VHCAGVGRGVFI 407
Db 1878 VHCAGVGRGVFI 1891

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## RESULT 7

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ID PTNE_HUMAN STANDARD; PRT; 1187 AA.
AC Q15678;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DB Protein tyrosine phosphatase, non-receptor type 14 (EC 3.1.3.48)
GN PTPN14 OR PEZ.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast carcinoma;
RX MEDLINE=95251727; PubMed=7733990;
RA Smith A.L., Mitchell P.J., Shipley J., Gusterson B.A., Rogers M.V.,
RA Crompton M.R.;
RT "Pez: a novel human cDNA encoding protein tyrosine phosphatase- and
RT ezrin-like domains."
RL Biochem. Biophys. Res. Commun. 209:959-965 (1995).
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -1- TISSUE SPECIFICITY: Expressed in a variety of human tissues
CC including kidney, skeletal muscle, lung and placenta.
CC -1- SIMILARITY: Contains 1 FERM domain.
CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
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DR EMBL: X82676; CAA57993.1; -
DR PIR: JCA155; JCA155.

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DR HSPP; P29350; IGWZ.
DR Genew; HGNC:9647; PTPN14.
DR MIM; 603153; -.
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; TAS.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR InterPro; IPR000268; Band 4.1.
DR InterPro; IPR000387; Tyr_PP.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00935; BAND4.1.
DR PRINTS; PR00700; PRTYPHPTASR.
DR SMART; SM00295; B4.1.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00660; FERM_1; 1.
DR PROSITE; PS00661; FERM_2; 1.
DR PROSITE; PS50057; FERM_3; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2.1.1.ase.
DR Structural protein; Cytoskeleton; Hydrolase.
FT DOMAIN 21 306 FERM.
FT DOMAIN 933 1187 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 1121 1121 PHOSPHOCYSTEINE INTERMEDIATE
FT DOMAIN 566 573 POLY-PRO.
FT DOMAIN 709 716 POLY-GLU.
SQ SEQUENCE 1187 AA; 135229 MW; 015760B75E3574E3 CRC64;

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Query Match 2.6%; Score 12; DB 1; Length 1187;
Best Local Similarity 100.0%; Pred. No. 0.0006;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 394 VHCAGVGRGV 405
Db 1119 VHCAGVGRGV 1130

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## RESULT 8

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ID PTNE_MOUSE STANDARD; PRT; 1189 AA.
AC Q62130;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DB Protein tyrosine phosphatase, non-receptor type 14 (EC 3.1.3.48)
GN PTPN14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CB-17-SCID; TISSUE=Thymus;
RX MEDLINE=94354845; PubMed=8074693;
RA Sawada M., Ogata M., Fujino Y., Hamaoka T.;
RT "cDNA cloning of a novel protein tyrosine phosphatase with homology
RT to cytoskeletal protein 4.1 and its expression in T-lymphocyte cells."
RL Biochem. Biophys. Res. Commun. 203:479-484 (1994).
CC -1- FUNCTION: MAY BE INVOLVED IN THE REGULATION OF T CELL DEVELOPMENT.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -1- TISSUE SPECIFICITY: Thymus; in cells of both hematopoietic and
CC non-hematopoietic origins.
CC -1- SIMILARITY: Contains 1 FERM domain.
CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
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FT CARBOHYD 685 685 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 691 691 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 725 725 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 838 838 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1238 AA; 136762 MW; 9394795DC016835 CR664;

Query Match 2.6%; Score 12; DB 1; Length 1238;
Best Local Similarity 100.0%; Pred. No. 0.00062;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 393 LVHCSAGVGRG 404
DB 1137 LVHCSAGVGRG 1148

RESULT 10
PTPJ_HUMAN STANDARD; PRT; 1337 AA.
ID Q12913; Q15255; Q8NRM2;
AC 01-NOV-1997 (Rel. 35, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase eta precursor (EC 3.1.3.48) (R-PTP-eta)
DE (HPTP eta) (Protein-tyrosine phosphatase receptor type J) (Density
DE enhanced phosphatase-1) (DEP-1) (CD148 antigen).
CM PTPRJ OR DEP1.
CS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95024024; PubMed=7937872;
RA Oestman A., Yang Q., Tonks N.R.;
RT "Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase,
RT is enhanced with increasing cell density."
RL Proc. Natl. Acad. Sci. U.S.A. 91:9680-9684(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95086212; PubMed=7994032;
RA Honda H., Inazawa J., Nishida J., Yazaki Y., Hirai H.;
RT "Molecular cloning, characterization, and chromosomal localization of
RT a novel protein-tyrosine phosphatase, HPTP eta."
RL Blood 84:4186-4194(1994).
RN [3]
RP SEQUENCE OF 33-1337 FROM N.A., AND VARIANTS COLON CANCER CYS-214 AND
RP PRO-276.
RC TISSUE=Colon;
RX MEDLINE=22084388; PubMed=12089527;
RA Rutvenkamp C.A.L., van Wezel T., Zanon C., Staessen A.P.M., Vlcek C.,
RA Csikos T., Klous A.M., Tripodis N., Petrakis A., Boerlgen L.,
RA Groot P.C., Lindman J., Mooi W.J., Meijer G.A., Scholten G.,
RA Dauveree H., Paces V., van Zanwijk N., van Ommen G.J.B., Demant P.;
RT "PTPJ is a candidate for the mouse colon-cancer susceptibility locus
RT Sccl and is frequently deleted in human cancers."
RL Nat. Genet. 31:299-300(2002).
RN [4]
RP FUNCTION: May contribute to the mechanism of contact inhibition of
RP cell growth.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- PTM: N- and O-glycosylated.
CC -1- DISEASE: Defects in PTPRJ are found in cancers of colon, lung, and
CC breast.
CC -1- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.
CC -1- SIMILARITY: Contains 5 fibronectin type III domains.
CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD148 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd148.htm".
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CC -----
DR EMBL; U10886; AAB36687.1; -
DR EMBL; D37781; BAA07035.1; -
DR EMBL; AF387844; AAM69432.1; JOINED.
DR EMBL; AF387823; AAM69432.1; JOINED.
DR EMBL; AF387824; AAM69432.1; JOINED.
DR EMBL; AF387825; AAM69432.1; JOINED.
DR EMBL; AF387826; AAM69432.1; JOINED.
DR EMBL; AF387827; AAM69432.1; JOINED.
DR EMBL; AF387828; AAM69432.1; JOINED.
DR EMBL; AF387829; AAM69432.1; JOINED.
DR EMBL; AF387830; AAM69432.1; JOINED.
DR EMBL; AF387831; AAM69432.1; JOINED.
DR EMBL; AF387832; AAM69432.1; JOINED.
DR EMBL; AF387833; AAM69432.1; JOINED.
DR EMBL; AF387834; AAM69432.1; JOINED.
DR EMBL; AF387835; AAM69432.1; JOINED.
DR EMBL; AF387836; AAM69432.1; JOINED.
DR EMBL; AF387837; AAM69432.1; JOINED.
DR EMBL; AF387838; AAM69432.1; JOINED.
DR EMBL; AF387839; AAM69432.1; JOINED.
DR EMBL; AF387840; AAM69432.1; JOINED.
DR EMBL; AF387841; AAM69432.1; JOINED.
DR EMBL; AF387842; AAM69432.1; JOINED.
DR EMBL; AF387843; AAM69432.1; JOINED.
DR PIR; I38670; I38670.
DR HSSP; P18052; 1YFO.
DR Genew; HGNC:9673; PTPRJ.
DR MIM; 600925; -
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. . .; TAS.
DR GO; GO:0007670; P:cell-cell signaling; TAS.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; TAS.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR001961; FN III.
DR InterPro; IPR000387; Tyr phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 6.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 8.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW Signal; Glycoprotein; Transmembrane; Repeat; Hydrolase;
KW Disease mutation.
FT SIGNAL 1 35
FT CHAIN 36 1337
FT DOMAIN 976 975
FT TRANSFEM 976 975
FT DOMAIN 997 1337
FT DOMAIN 119 199
FT DOMAIN 366 446
FT DOMAIN 454 532
FT DOMAIN 540 615
FT DOMAIN 626 710
FT DOMAIN 1065 1337
FT ACT_SITE 1239 1239
FT CARBOHYD 72 72
FT CARBOHYD 82 82
FT CARBOHYD 93 93
FT CARBOHYD 104 104
FT CARBOHYD 142 142
FT CARBOHYD 172 172
FT CARBOHYD 192 192
FT CARBOHYD 231 231

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FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 278 278 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 342 342 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 376 376 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 501 501 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 525 525 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 536 536 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 582 582 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 603 603 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 618 618 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 666 666 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 761 761 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 772 772 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 784 784 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 790 790 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 824 824 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 910 910 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 937 937 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT VARIANT 214 214 R -> C (in colon cancer; somatic mutation)
FT VARIANT 276 276 /FtId=VAR_015905.
O -> P (in colon cancer; somatic mutation)
FT CONFLICT 261 261 /FtId=VAR_015906.
G -> D (IN REF. 1).
FT CONFLICT 918 929 YNGLIEPLGYSYR -> LOWEAGTGLLP (IN REF. 2).
SQ SEQUENCE 1337 AA; 145926 MW; E6752D521C4BA8F CRC64;

Query Match 2.6%; Score 12; DB 1; Length 1337;
Best Local Similarity 100.0%; Pred. No. 0.0067;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 393 LVHCSAGVGRG 404
Db 1236 LVHCSAGVGRG 1247

RESULT 11
PTPG_MOUSE STANDARD; PRT; 1442 AA.
AC 005959;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase gamma precursor (EC 3.1.3.48) (R-PTP-gamma).
GN PTPRG.
OS Mus musculus (Mouse).
CC Bukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93180796; PubMed=8382771;
RA Barnes G., Silvennoinen O., Shaanan B., Honneger A.M., Canoll P.D.,
RA D'Amico P., Morse B., Levy U.B., Laforgia S., Huebner K.,
RA Musacchio J.M., Sap J., Schlessinger U.;
RT Identification of a carbonic anhydrase-like domain in the
RT extracellular region of RPTP gamma defines a new subfamily of receptor
RT tyrosine phosphatases";
RL Mol. Cell. Biol. 13:1497-1506(1993).
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H2O = protein
CC tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -1- TISSUE SPECIFICITY: Detected in brain, lung, kidney, heart, liver,

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CC skeletal muscle, spleen and testes. It is developmentally
CC regulated in the brain.
CC -1- SIMILARITY: Contains 1 eukaryotic-type carbonic anhydrase domain.
CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
CC -1- SIMILARITY: Contains 1 fibronectin type III domain.
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; L09562; AAA40022.1; -
DR PIR; B48148; B48148.
DR HSSP; P18052; 1YFO.
DR MGD; MGI:97814; Ptpg.
DR InterPro; IPR001148; Suk Coanhd.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR000387; Tyr_Pp.
DR InterPro; IPR000242; Tyr_Pp.
DR Pfam; PF00194; carb_anhydrase; 1.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00102; Y-phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR ProDom; PD000865; Suk Coanhd; 1.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00363; TYR_PHOSPHATASE 1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE 2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE PTP; 2.
KW Glycoprotein; Transmembrane; Hydrolyase; Repeat; Signal.
BY SIMILARITY.
FT SIGNAL 1 19
FT GRAIN 20 1442
FT TRANSSEM 20 733
FT DOMAIN 734 759
FT DOMAIN 760 1442
FT DOMAIN 56 322
FT DOMAIN 347 441
FT DOMAIN 866 1122
FT DOMAIN 1123 1442
FT ACT_SITE 1057 1057
FT SITE 1348 1348
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 359 359 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 444 444 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 719 719 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 1442 AA; 161242 MW; 588715568FBC08 CRC64;

Query Match 2.6%; Score 12; DB 1; Length 1442;
Best Local Similarity 100.0%; Pred. No. 0.00072;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 393 LVHCSAGVGRG 404
Db 1054 LVHCSAGVGRG 1065

RESULT 12
PTPG_HUMAN STANDARD; PRT; 1445 AA.
AC P23470; Q15623;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase gamma precursor (EC 3.1.3.48) (R-PTP-gamma).
GN PTPRG.

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OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93180796; PubMed=8382771;  
 RA Barnea G., Silvennoinen O., Shaan B., Honneger A.M., Canci P.D.,  
 RA D'Ustachio P., Morse B., Levy J.B., Laforgia S., Huebner K.,  
 RA Musacchio J.M., Sap J., Schlessinger J.;  
 RT "Identification of a carbonic anhydrase-like domain in the  
 RT extracellular region of RPRP gamma defines a new subfamily of  
 RT receptor tyrosine phosphatases."  
 RL Mol. Cell. Biol. 13:1497-1506(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96429999; PubMed=8833149;  
 RA Kastury K., Ohta M., Lasota J., Moir D., Dorman T., Laforgia S.,  
 RA Druck T., Huebner K.;  
 RT "Structure of the human receptor tyrosine phosphatase gamma gene  
 RT (PTPRG) and relation to the familial RCC t(3;8) chromosome  
 RT translocation.";  
 RL Genomics 32:225-235(1996).  
 RN [3]  
 RP SEQUENCE OF 836-1445 FROM N.A.  
 RX MEDLINE=91006018; PubMed=2170109;  
 RA Krieger N.X., Streuli M., Saito H.;  
 RT "Structural diversity and evolution of human receptor-like protein  
 RT tyrosine phosphatases.";  
 RL EMBO J. 9:3241-3252(1990).  
 RN [4]  
 RP SEQUENCE OF 874-1118 AND 1175-1409 FROM N.A.  
 RX MEDLINE=90384936; PubMed=2169617;  
 RA Kadian R., Morse B., Huebner K., Croce C., Hawk R., Ravera M.,  
 RA Ricca G., Jaye M., Schlessinger J.;  
 RT "Cloning of three human tyrosine phosphatases reveals a multigene  
 RT family of receptor-linked protein-tyrosine-phosphatases expressed in  
 RT brain.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:7000-7004(1990).  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Probable).  
 CC -1- TISSUE SPECIFICITY: Found in a variety of tissues. It is  
 CC developmentally regulated in the brain (By similarity).  
 CC -1- SIMILARITY: Contains 1 eukaryotic-type carbonic anhydrase domain.  
 CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
 CC -1- SIMILARITY: Contains 1 fibronectin type III domain.  
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 CC -----  
 DR EMBL; L09247; AAA60224.1; -;  
 DR EMBL; U46116; AAC50439.1; JOINED.  
 DR EMBL; U46089; AAC50439.1; JOINED.  
 DR EMBL; U46091; AAC50439.1; JOINED.  
 DR EMBL; U46092; AAC50439.1; JOINED.  
 DR EMBL; U46093; AAC50439.1; JOINED.  
 DR EMBL; U46094; AAC50439.1; JOINED.  
 DR EMBL; U46095; AAC50439.1; JOINED.  
 DR EMBL; U46096; AAC50439.1; JOINED.  
 DR EMBL; U46097; AAC50439.1; JOINED.  
 DR EMBL; U46098; AAC50439.1; JOINED.  
 DR EMBL; U46099; AAC50439.1; JOINED.  
 DR EMBL; U46100; AAC50439.1; JOINED.  
 DR EMBL; U46101; AAC50439.1; JOINED.

DR EMBL; U46102; AAC50439.1; JOINED.  
 DR EMBL; U46103; AAC50439.1; JOINED.  
 DR EMBL; U46104; AAC50439.1; JOINED.  
 DR EMBL; U46105; AAC50439.1; JOINED.  
 DR EMBL; U46106; AAC50439.1; JOINED.  
 DR EMBL; U46107; AAC50439.1; JOINED.  
 DR EMBL; U46108; AAC50439.1; JOINED.  
 DR EMBL; U46109; AAC50439.1; JOINED.  
 DR EMBL; U46110; AAC50439.1; JOINED.  
 DR EMBL; U46111; AAC50439.1; JOINED.  
 DR EMBL; U46112; AAC50439.1; JOINED.  
 DR EMBL; U46113; AAC50439.1; JOINED.  
 DR EMBL; U46114; AAC50439.1; JOINED.  
 DR EMBL; U46115; AAC50439.1; JOINED.  
 DR EMBL; X54132; CA43067.1; -;  
 DR PIR; A48148; A48148.  
 DR HSSP; P18052; 1YPO.  
 DR Genew; HGNC:9671; PTPRG.  
 DR MTM; 176886; -;  
 DR GO; GO:0005687; C: integral to plasma membrane; TAS.  
 DR GO; GO:0005901; P: transmembrane receptor protein tyrosine pho. . .; TAS.  
 DR GO; GO:0007169; P: transmembrane receptor protein tyrosine kin. . .; TAS.  
 DR InterPro; IPR001148; Euk\_COand.  
 DR InterPro; IPR008957; FN\_III-like.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR000242; Tyr\_Pp.  
 DR InterPro; IPR000387; Tyr\_Pp.  
 DR Pfam; PF00194; carb\_anhydase; 1.  
 DR Pfam; PF00641; Fns; 1.  
 DR Pfam; PF00102; Y\_Posphatase; 2.  
 DR PRINTS; PR00700; PRTPHPTASE.  
 DR ProDom; PD000865; Euk\_COand; 1.  
 DR SMART; SM00194; PTPC; 2.  
 DR PROSITE; PS00383; TYR\_PHSPTASE\_1; 1.  
 DR PROSITE; PS0056; TYR\_PHSPTASE\_2; 2.  
 DR PROSITE; PS0055; TYR\_PHSPTASE\_PTP; 2.  
 DR GlycoProtein; Transmembrane; Hydrolyase; Phosphorylation; Repeat;  
 KW Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 1445  
 FT DOMAIN 20 736  
 FT TRANSMEM 737 762  
 FT DOMAIN 763 1445  
 FT DOMAIN 56 322  
 FT DOMAIN 347 441  
 FT DOMAIN 869 1125  
 FT DOMAIN 1126 1445  
 FT ACT\_SITE 1060 1060  
 FT SITE 1351 1351  
 FT CARBOHYD 109 109  
 FT CARBOHYD 113 113  
 FT CARBOHYD 156 156  
 FT CARBOHYD 359 359  
 FT CARBOHYD 444 444  
 FT CARBOHYD 619 619  
 FT CARBOHYD 631 631  
 FT CARBOHYD 722 722  
 FT CARBOHYD 80 80  
 FT CONFLICT 92 92  
 FT CONFLICT 549 549  
 FT CONFLICT 756 756  
 FT CONFLICT 1407 1407  
 SQ SEQUENCE 1445 AA; 162058 MW; 350FB90DC94E80BD CRC64;  
 Query Match 2.6%; Score 12; DB 1; Length 1445;  
 Best local Similarity 100.0%; Pred. No. 0.00072;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 393 LVHCSAGVGRG 404  
 Db 1057 LVHCSAGVGRG 1068

RESULT 13  
 PTP6\_DROME STANDARD; PRT; 1462 AA.  
 ID PTP6\_DROME STANDARD; PRT; 1462 AA.  
 AC P16620;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein-tyrosine phosphatase DPTP precursor (EC 3.1.3.48) (Protein-tyrosine-phosphate phosphohydrolase).  
 GN PTP69D OR DPTP.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_TaxID=7227;  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90046860; PubMed=2554325;  
 RA Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;  
 RT "A family of receptor-linked protein tyrosine phosphatases in humans and Drosophila.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).  
 CC -1- FUNCTION: It is possible that DPTP is a cell adhesion receptor.  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.  
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.  
 CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@sb-sib.ch](mailto:license@sb-sib.ch)).  
 CC  
 CC EMBL: M27699; AAA28842.1; -;  
 CC PIR: B36182; B36182.  
 CC HSSP: P18052; 1YRC.  
 CC FLYBASE: FBgn0014007; Ptp69D.  
 CC GO: GO:0004725; P:Protein tyrosine phosphatase activity; IDA.  
 CC GO: GO:0007415; P:defasciculation of motor neuron; IGI.  
 CC GO: GO:0008045; P:motor axon guidance; IGI.  
 CC GO: GO:0006470; P:protein amino acid dephosphorylation; IDA.  
 CC InterPro: IPR006957; FN\_III-like.  
 CC InterPro: IPR003961; FN\_III.  
 CC InterPro: IPR007110; IG\_1like.  
 CC InterPro: IPR003598; IG\_c2.  
 CC InterPro: IPR000387; Tyr\_phosphatase.  
 CC InterPro: IPR000242; Tyr\_PP.  
 CC Pfam: PF00041; fn3; 3.  
 CC Pfam: PF00047; Ig; 2.  
 CC Pfam: PF00102; Y\_phosphatase; 2.  
 CC PRINTS: PR00700; PRTYPHATASE.  
 CC SMART: SM00060; FN3; 3.  
 CC SMART: SM00408; IGC2; 1.  
 CC SMART: SM00194; PTPC; 2.  
 CC PROSITE: PS50835; IG\_LIKE; 2.  
 CC PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 2.  
 CC PROSITE: PS50056; TYR\_PHOSPHATASE\_2; 2.  
 CC PROSITE: PS50055; TYR\_PHOSPHATASE\_PTP; 2.  
 CC HydroLase; Receptor; Glycoprotein; Signal; Transmembrane; Cell adhesion; Immunoglobulin domain; Repeat.  
 KM  
 FT SIGNAL 1 23  
 FT CRAIN 24 1462 PROTEIN-TYROSINE PHOSPHATASE DPTP.  
 FT DOMAIN 24 805 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 806 823 POTENTIAL.  
 FT DOMAIN 824 1462 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 24 125 IG-LIKE C2-TYPE 1.

FE DOMAIN 131 230 IG-LIKE C2-TYPE 2.  
 FE 332 437 FIBRONECTIN TYPE-III 1.  
 FE 438 538 FIBRONECTIN TYPE-III 2.  
 FE 912 1165 PROTEIN-TYROSINE PHOSPHATASE 1.  
 FE 1208 1459 PROTEIN-TYROSINE PHOSPHATASE 2.  
 FE 1097 1097 PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).  
 FE ACT\_SITE 1097 1097 PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).  
 FE ACT\_SITE 1391 1391 PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).  
 FE DISULFID 45 112 POTENTIAL.  
 FE DISULFID 154 214 POTENTIAL.  
 FE CARBOHYD 40 40 (POTENTIAL).  
 FE CARBOHYD 58 58 (POTENTIAL).  
 FE CARBOHYD 64 64 (POTENTIAL).  
 FE CARBOHYD 85 85 (POTENTIAL).  
 FE CARBOHYD 105 105 (POTENTIAL).  
 FE CARBOHYD 109 109 (POTENTIAL).  
 FE CARBOHYD 119 119 (POTENTIAL).  
 FE CARBOHYD 162 162 (POTENTIAL).  
 FE CARBOHYD 191 191 (POTENTIAL).  
 FE CARBOHYD 196 196 (POTENTIAL).  
 FE CARBOHYD 209 209 (POTENTIAL).  
 FE CARBOHYD 255 255 (POTENTIAL).  
 FE CARBOHYD 288 288 (POTENTIAL).  
 FE CARBOHYD 302 302 (POTENTIAL).  
 FE CARBOHYD 429 429 (POTENTIAL).  
 FE CARBOHYD 442 442 (POTENTIAL).  
 FE CARBOHYD 451 451 (POTENTIAL).  
 FE CARBOHYD 516 516 (POTENTIAL).  
 FE CARBOHYD 613 613 (POTENTIAL).  
 FE CARBOHYD 701 701 (POTENTIAL).  
 FE CARBOHYD 755 755 (POTENTIAL).  
 FE SEQUENCE 1462 AA; 167411 MW; F8091D69E88230EB CRC64;  
 SQ  
 Query Match 2.6%; Score 12; DB 1; Length 1462;  
 Best Local Similarity 100.0%; Pred. No. 0.00073;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 393 LVHCSAGVGRG 404  
 DB 1094 LVHCSAGVGRG 1105  
 RESULT 14  
 PTPV\_MOUSE STANDARD; PRT; 1705 AA.  
 ID PTPV\_MOUSE STANDARD; PRT; 1705 AA.  
 AC P70289;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Receptor-type protein-tyrosine phosphatase V precursor (EC 3.1.3.48) (Embryonic stem cell protein-tyrosine phosphatase) (ES cell phosphatase).  
 DE DE (Embryonic stem cell protein-tyrosine phosphatase) (ES cell phosphatase).  
 GN PTPRV OR ESP.  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryonic stem cells;  
 RX MEDLINE=97109513; PubMed=8951793;  
 RA Lee K., Nichols J., Smith A.;  
 RT "Identification of a developmentally regulated protein tyrosine phosphatase in embryonic stem cells that is a marker of pluripotential epiblast and early mesoderm.";  
 RT Mech. Dev. 59:153-164(1996).  
 RL Mech. Dev. 59:153-164(1996).  
 RN  
 RP ERRATUM.  
 RA Lee K., Nichols J., Smith A.;  
 RL Mech. Dev. 61:213-215(1996).  
 CC -1- FUNCTION: May play a role in the maintenance of pluripotency. Down-regulated during differentiation.



DR EMBL: L36884; AAA63911.1; -.  
DR HSP: P18052; TYRO.  
DR InterPro: IPR008957; FN\_III-like.  
DR InterPro: IPR003964; FN\_III.  
DR InterPro: IPR000387; TYR\_phosphatase.  
DR InterPro: IPR000242; Tyr\_PP.  
DR Pfam: PF00041; En3; 7.  
DR Pfam: PF00102; Y\_phosphatase; 1.  
DR PRINTS: PR00700; PRTYPHPTASE.  
DR SMART: SM00060; FN3; 8.  
DR SMART: SM00194; FTRC; 1.  
DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 1.  
DR PROSITE: PS50056; TYR\_PHOSPHATASE\_2; 1.  
DR PROSITE: PS50055; TYR\_PHOSPHATASE\_PP; 2.  
KW Hydrolyase; Transmembrane; Repeat; Signal; Glycoprotein;  
KW Alternative splicing.  
FT SIGNAL 1 17  
FT CHAIN 18 1711  
FT DOMAIN 18 1074  
FT TRANSMEM 1075 1095  
FT DOMAIN 1096 1711  
FT DOMAIN 125 124  
FT DOMAIN 125 215  
FT DOMAIN 216 303  
FT DOMAIN 304 392  
FT DOMAIN 393 470  
FT DOMAIN 471 562  
FT DOMAIN 563 652  
FT DOMAIN 653 741  
FT DOMAIN 742 830  
FT DOMAIN 831 921  
FT DOMAIN 1150 1418  
FT DOMAIN 1419 1711  
FT ACT\_SITE 1350 1350  
FT CARBOHYD 42 42  
FT CARBOHYD 74 74  
FT CARBOHYD 89 89  
FT CARBOHYD 117 117  
FT CARBOHYD 174 174  
FT CARBOHYD 239 239  
FT CARBOHYD 259 259  
FT CARBOHYD 431 431  
FT CARBOHYD 570 570  
FT CARBOHYD 620 620  
FT CARBOHYD 649 649  
FT CARBOHYD 663 663  
FT CARBOHYD 737 737  
FT CARBOHYD 851 851  
FT CARBOHYD 882 882  
FT CARBOHYD 970 970  
FT CARBOHYD 982 982  
SQ SEQUENCE 1711 AA; 187292 MW; 0F04D2D1A47A18A0 CRC64;  
Query Match 2.6%; Score 12; DB 1; Length 1711;  
Best Local Similarity 100.0%; Pred. No. 0.00084;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 393 LVHCSAGVGRG 404  
DB 1347 LVHCSAGVGRG 1358

Search completed: June 18, 2004, 19:47:44  
Job time : 17 secs

GenCore version 5.1.6  
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OK protein - protein search, using sw model

Run on: June 18, 2004, 19:44:34 ; Search time 45 Seconds  
(without alignments)  
3246.332 Million cell updates/sec

Title: US-09-095-478a-6  
Perfect score: 463  
Sequence: 1 MSSEPRKRYKGTGRNDDEEG.....QYQFCEYIVLEVQNLALY 463

Scoring table: GIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTRMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacterioplasmid:\*  
17: sp\_archaeoplasmid:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	383	82.7	426	11	055082
2	19	4.1	398	4	Q9Y406
3	15	3.2	336	11	Q9CWO7
4	15	3.2	446	5	Q9Y1X4
5	15	3.2	758	11	07TWG1
6	15	3.2	1024	4	Q8W29
7	14	3.0	24	11	088571
8	14	3.0	24	11	088570
9	14	3.0	79	11	088570
10	14	3.0	93	11	088570
11	14	3.0	134	4	Q9UM23
12	14	3.0	183	5	Q9Y1X3
13	14	3.0	192	11	08C922
14	14	3.0	460	11	062817
15	14	3.0	468	13	Q91BA5
16	14	3.0	468	13	Q91BA2

17	14	3.0	468	13	Q91BA0
18	14	3.0	598	13	Q9Y0Y5
19	14	3.0	582	11	Q64696
20	14	3.0	615	13	Q91A18
21	14	3.0	749	11	Q8R169
22	14	3.0	857	13	Q9Y0Y4
23	14	3.0	1131	4	Q723X4
24	14	3.0	1231	5	Q17024
25	14	3.0	1254	11	Q8YBV0
26	14	3.0	1359	4	Q75870
27	14	3.0	1459	13	Q90815
28	14	3.0	1501	11	Q9QW00
29	14	3.0	1501	11	Q77T17
30	14	3.0	1502	4	Q9UM81
31	14	3.0	1788	13	Q91A10
32	14	3.0	1863	11	Q64605
33	14	3.0	1887	11	Q9QW67
34	14	3.0	1894	11	Q64487
35	14	3.0	1896	13	Q91A11
36	14	3.0	1898	4	Q86W50
37	14	3.0	1898	11	Q9EQ17
38	14	3.0	1898	11	Q64604
39	14	3.0	1904	11	Q64699
40	14	3.0	2051	5	Q44328
41	14	3.0	2302	11	Q88488
42	14	2.8	469	5	Q9N111
43	13	2.6	469	13	Q9N108
44	12	2.6	112	11	Q91TJ6
45	12	2.6	184	5	Q02048

## ALIGNMENTS

### RESULT 1

055082 ID 055082 PRELIMINARY; PRT; 426 AA.  
AC 055082;  
DT 01-JUN-1998 (TREMBLrel. 06, Created)  
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Protein-tyrosine-phosphatase (EC 3.1.3.48).  
GN PRPN20.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OC NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RX MEDLINE=98070510; PubMed=9407093;  
RA Ohsugi M., Kuramochi S., Matsuda S., Yamamoto T.;  
RT "Molecular cloning and characterization of a novel cytoplasmic  
RT protein-tyrosine phosphatase that is specifically expressed in  
RT spermatocytes.";  
RT J Biol. Chem. 272:33092-33099(1997).  
RL T Biol. Chem. 272:33092-33099(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RX MEDLINE=2354683; PubMed=12466851;  
RA The FANTOM Consortium.  
RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
DR EMBL; D64141; BAA23761.1; -.  
DR EMBL; AK029493; BAC26476.1; -.  
DR HSSP; Q06124; 2SHP.  
DR MGD; MGI:1196295; Ptpn20.  
DR GO; GO:0016787; F:hydrolysis activity; IEA.  
DR GO; GO:0004727; F:phosphorylated protein tyrosine phosphatase act. .; IEA.  
DR GO; GO:0004700; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR00387; Tyr\_phosphatase.

DR InterPro: IPR000242; TYR\_PP.  
 DR Pfam: PF00102; Y\_phosphatase; 1.  
 DR PRINTS: PRO0700; PRTYPHPTASE.  
 DR SMART: SM00194; PTPc; 1.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE: PS50056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE: PS50055; TYR\_PHOSPHATASE\_PTP; 1.  
 DR Hydrolase.  
 SQ SEQUENCE 426 AA; 49118 MW; 2835FB13379502F4 CRC64;

Query Match 82.7%; Score 383; DB 11; Length 426;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 IFGNKNSENVKPSHSLSPDSEKYLVEPLESDTDEIVMDVSDRLNRNNSMDSETAG 140  
 DB 44 IFGNKNSENVKPSHSLSPDSEKYLVEPLESDTDEIVMDVSDRLNRNNSMDSETAG 103  
 QY 141 PSKTVSPVLSGSSSRSLKSTETSVSKELTQLAQIRPLFNSSASAMRDCLNTLQKREL 200  
 DB 104 PSKTVSPVLSGSSSRSLKSTETSVSKELTQLAQIRPLFNSSASAMRDCLNTLQKREL 163  
 QY 201 DIREFLEDMTLPDDFNSGNTLQNRDKRRDILPYDSTRVPLGKNDYINASYRIY 260  
 DB 164 DIREFLEDMTLPDDFNSGNTLQNRDKRRDILPYDSTRVPLGKNDYINASYRIY 223  
 QY 261 NEESEYFIATQGLPETIEDFWQVLENNCNVIAITREIEGVIKCYSTWPISLKEPL 320  
 DB 224 NEESEYFIATQGLPETIEDFWQVLENNCNVIAITREIEGVIKCYSTWPISLKEPL 283  
 QY 321 EFHFSVLEFHTQYFTVAVPOIVKSKSGCKVCKLQPTKMPDGTSPASAPFIKYV 380  
 DB 284 EFHFSVLEFHTQYFTVAVPOIVKSKSGCKVCKLQPTKMPDGTSPASAPFIKYV 343  
 QY 381 RYVKRSHTGPLVHCSAGVAGRTGVCVDVFAIEKNVSPFIMNTVITQMRKRCQMIQ 440  
 DB 344 RYVKRSHTGPLVHCSAGVAGRTGVCVDVFAIEKNVSPFIMNTVITQMRKRCQMIQ 403  
 QY 441 TKEOYPCYEIVLEVLQNTLLLY 463  
 DB 404 TKEOYPCYEIVLEVLQNTLLLY 426

## RESULT 2

QY406 PRELIMINARY; PRT; 398 AA.  
 AC QY406;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 GN DKFZPS66K0524.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID:9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Ansgore W., Wikner U., Mewes H.W., Gassenhuber J., Wiemann S.;  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL050040; CAB43248.1; -.  
 DR PIR; T08716; T08716.  
 DR HSSP; Q06124; 2SHP.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro: IPR000387; TYR\_phosphatase.  
 DR InterPro: IPR000242; TYR\_PP.  
 DR Pfam; PF00102; Y\_phosphatase; 1.  
 DR PRINTS; PRO0700; PRTYPHPTASE.  
 DR SMART; SM00194; PTPc; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.

DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 1.  
 DR Hypothetical protein; Hydrolase.  
 FT NON TER  
 SQ SEQUENCE 398 AA; 45690 MW; 857AAD03747870A2 CRC64;

Query Match 4.1%; Score 19; DB 4; Length 398;  
 Best Local Similarity 100.0%; Pred. No. 2,3e-11;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 KNRRIPLPYDSTRVPLGK 247  
 DB 164 KNRRIPLPYDSTRVPLGK 182

## RESULT 3

QY406 PRELIMINARY; PRT; 336 AA.  
 AC QY406;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE PTP-RL10b.  
 GN PTPN21.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID:10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57-Bl6; TISSUE=Testis;  
 RA Nishiyama H., Higashitsuji H., Fujita J.;  
 RT "Expression of mouse PTP-RL10 isoforms in testis."  
 RE Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; D83072; BAA19740.1; -.  
 DR HSSP; P29350; 1GMZ.  
 DR MGD; MGI:1344406; Ptpn21.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro: IPR000387; TYR\_phosphatase.  
 DR InterPro: IPR000242; TYR\_PP.  
 DR Pfam; PF00102; Y\_phosphatase; 1.  
 DR PRINTS; PRO0700; PRTYPHPTASE.  
 DR SMART; SM00194; PTPc; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 1.  
 DR Hydrolase.  
 SQ SEQUENCE 336 AA; 38503 MW; 679B68360C39PFD CRC64;

Query Match 3.2%; Score 15; DB 11; Length 336;  
 Best Local Similarity 100.0%; Pred. No. 4,3e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 PLVHCSAGVAGRTGV 405  
 DB 265 PLVHCSAGVAGRTGV 279

## RESULT 4

QY414 PRELIMINARY; PRT; 446 AA.  
 AC QY414;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE SPTPS (Fragment).  
 OS Eukaryota; Metazoa; Porifera; Demosporangiae; Ceractinomorpha;  
 OC Eukaryota; Metazoa; Porifera; Demosporangiae; Ceractinomorpha;  
 OC Haptoclerida; Spongillidae; Ephydatia.  
 OC NCBI\_TaxID:31330;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=99245376; PubMed=10229569;  
 RA Ono K., Suga H., Iwabe N., Kuma K., Miyata T.;  
 RT "Multiple protein tyrosine phosphatases in sponges and explosive gene  
 duplication in the early evolution of animals before the parazoan-  
 eumetazoan split.";  
 RT J. Mol. Evol. 48:654-662(1999).  
 DR EMBL: AB019127; BAA82560.1; -.  
 DR HSP: P18052; IYFO.  
 DR GO: GO:0016787; F:Hydrolase activity; IEA.  
 DR GO: GO:0004725; P:Protein tyrosine phosphatase activity; IEA.  
 DR GO: GO:0006470; P:Protein amino acid dephosphorylation; IEA.  
 DR InterPro: IPR000387; TYR\_P.  
 DR InterPro: IPR000242; TYR\_PP.  
 DR Pfam: PF00102; Y\_ProteinPhatase. 2.  
 DR PRINTS: PR00700; ERTYPPHPTASE.  
 DR SMART: SM00194; PTPc. 2.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE: PS50056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE: PS50055; TYR\_PHOSPHATASE\_PTP; 2.  
 KM Hydrolase.  
 FT NON TER  
 SQ SEQUENCE 446 AA; 50165 MW; 985B0AF6168DF77C CRC64;  
 Query Match 3.2%; Score 15; DB 5; Length 446;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 390 GPLVHCSAGVGRGTG 404  
 DB 102 GPLVHCSAGVGRGTG 116  
 RESULT 5  
 Q7TMG1 PRELIMINARY; PRT; 758 AA.  
 AC Q7TMG1;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Protein tyrosine phosphatase, non-receptor type 21 (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C2ECH II; TISSUE=Breast tumor;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pange C.,  
 RA Raha S.S., Loquajano N.A., Peters G.U., Abramson R.D., Mulhally S.J.,  
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakeley R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzyzanski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C2ECH II; TISSUE=Breast tumor;  
 RA Strausberg R.;

RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC055942; AAH55942.1; -.  
 KM Receptor.  
 FT NON TER  
 SQ SEQUENCE 758 AA; 85514 MW; 6C3CBA40C026B037 CRC64;  
 Query Match 3.2%; Score 15; DB 11; Length 758;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 391 PLTVHCSAGVGRGTG 405  
 DB 687 PLTVHCSAGVGRGTG 701  
 RESULT 6  
 Q8WX29 PRELIMINARY; PRT; 1024 AA.  
 AC Q8WX29;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE D11175B15.2 (Protein tyrosine phosphatase, non-receptor type 21)  
 DE (Fragment).  
 GN Homo sapiens (Human).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Howden P.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL353786; CAD19000.1; -.  
 DR GO: GO:0005856; C:Cytoskeleton; IEA.  
 DR GO: GO:0016787; F:Hydrolase activity; IEA.  
 DR GO: GO:0004725; P:Protein tyrosine phosphatase activity; IEA.  
 DR GO: GO:0004872; P:Protein tyrosine phosphatase activity; IEA.  
 DR GO: GO:0006470; P:Protein amino acid dephosphorylation; IEA.  
 DR InterPro: IPR000299; Band 4.1.  
 DR InterPro: IPR000387; TYR\_ProteinPhatase.  
 DR InterPro: IPR000242; TYR\_PP.  
 DR Pfam: PF00102; Y\_ProteinPhatase. 1.  
 DR PRINTS: PR00700; ERTYPPHPTASE.  
 DR SMART: SM00194; PTPc. 1.  
 DR PROSITE: PS00661; FERM\_2; 1.  
 DR PROSITE: PS50057; FERM\_3; 1.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE: PS50056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE: PS50055; TYR\_PHOSPHATASE\_PTP; 1.  
 KM Hydrolase; Receptor.  
 FT NON TER  
 SQ SEQUENCE 1024 AA; 115763 MW; C702F90D6AF38AB CRC64;  
 Query Match 3.2%; Score 15; DB 4; Length 1024;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 391 PLTVHCSAGVGRGTG 405  
 DB 953 PLTVHCSAGVGRGTG 967  
 RESULT 7  
 O88571 PRELIMINARY; PRT; 24 AA.  
 AC O88571;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Protein tyrosine phosphatase PTP-GWCI (Fragment).  
 GN PTPRO.  
 OS Mus spretus (Western wild mouse).



OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxId=10096;
RN	(1)
RP	SEQUENCE FROM N.A.
RX	MEDLINE=98395110; PubMed=9727007;
RA	Wright M.B., Hugo C., Seifert R., Diatche C.M., Bowen-Pope D.F.,
RT	"Proliferating and migrating mesangial cells responding to injury
RT	express a novel receptor protein-tyrosine phosphatase in experimental
RT	mesangial proliferative glomerulonephritis.";
RL	J. Biol. Chem. 273:23928-23937(1998).
DR	EMBL; AF073999; AAC34822.1; -
DR	MCD; MGI:1096349; Pcpqg.
DR	GO; GO:0016787; F:hydrolyase activity; IEA.
DR	GO; GO:0004721; F:protein phosphatase activity; IEA.
DR	GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR	InterPro; IPR000387; TYR_phosphatase.
DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR	PROSITE; PSS0056; TYR_PHOSPHATASE_2; 1.
KW	Hydrolase.
FT	NON_TER
FT	NON_TER
SQ	SEQUENCE 24 AA; 2483 MW; 7E81ASFBE2BC2E2B CRC64;
QY	Query Match 394 VHCSAGVGTGVFI 407                     Best Local Similarity 100.0%; Score 14; DB 11; Length 24; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Dd	10 VHCSAGVGTGVFI 23
RESULT 8	
O88570	PRELIMINARY; PRF; 24 AA.
ID O88570;	
AC O88570;	
DT 01-NOV-1998 (TREMblrel. 08, Created)	
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)	
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)	
DE Protein tyrosine phosphatase xPTP-GMCI (Fragment).	
GN PTPO.	
OS Mus musculus (Mouse).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX NCBI_TaxId=10090;	
RN (1)	
RP SEQUENCE FROM N.A.	
RZ STRAIN=C57BL/6J;	
RX MEDLINE=98395110; PubMed=9727007;	
RA Wright M.B., Hugo C., Seifert R., Dische C.M., Bowen-Pope D.F.,	
RT "Proliferating and migrating mesangial cells responding to injury	
RT express a novel receptor protein-tyrosine phosphatase in experimental	
RT mesangial proliferative glomerulonephritis.";	
RL J. Biol. Chem. 273:23928-23937(1998).	
DR EMBL; AF073998; AAC34822.1; -	
DR MCD; MGI:1096349; Pcpqg.	
DR GO; GO:0016787; F:hydrolyase activity; IEA.	
DR GO; GO:0004721; F:protein phosphatase activity; IEA.	
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.	
DR InterPro; IPR000387; TYR_phosphatase.	
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.	
DR PROSITE; PSS0056; TYR_PHOSPHATASE_2; 1.	
KW Hydrolase.	
FT NON_TER	1
FT NON_TER	24
SQ SEQUENCE 24 AA; 2483 MW; 7E81ASFBE2BC2E2B CRC64;	
QY	Query Match 394 VHCSAGVGTGVFI 407                     Best Local Similarity 100.0%; Score 14; DB 11; Length 24; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0
394 VHCSAGVGTGVFI 407	

DB	10	VHCSAGVGRGVFI	23
RESULT 9			
Q8CC23	PRELIMINARY;	PRF;	79 AA.
ID	Q8CC23		
AC	Q8CC23;		
DT	01-MAR-2003 (TrEMBLrel. 23, Created)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Unknown EST (Fragment).		
GN	PTPRD.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Diencephalon;		
RC	MEDLINE=22354683; PubMed=12466851;		
RA	The FANTOM Consortium,		
RT	"Analysis of the mouse transcriptome based on functional annotation of		
RL	60,770 full-length cDNAs."		
RL	Nature 420:563-573(2002).		
DR	EMBL; AK034067; BAC28569.1; -.		
DR	MGI; MGI:97812; Ptpcd.		
DR	GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.		
DR	GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.		
DR	InterPro; IPR000387; PTPC motif.		
DR	InterPro; IPR000242; Tyr_Pp.		
DR	Pfam; PF00102; Y_phosphatase; 1.		
DR	PRINTS; PR00700; PTPPHPTASE.		
DR	SMART; SM00404; PTPC motif; 1.		
DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.		
DR	PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.		
DR	PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.		
FT	NON TER		
SC	SEQUENCE 79 AA; 8970 MW; EA7CAE6839241155 CRC64;		
Query Match	3.0%; Score 14; DB 11; Length 79;		
Best Local Similarity	100.0%; Freq. No. 1,4e-06;		
Matches 14; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
QY	394 VHCSAGVGRGVFI 407		
DB	9 VHCSAGVGRGVFI 22		
RESULT 10			
Q8CC54	PRELIMINARY;	PRF;	93 AA.
ID	Q8CC54		
AC	Q8CC54;		
DT	01-MAR-2003 (TrEMBLrel. 23, Created)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Unknown EST (Fragment).		
GN	PTPRD.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Diencephalon;		
RC	MEDLINE=22354683; PubMed=12466851;		
RA	The FANTOM Consortium,		
RT	"Analysis of the mouse transcriptome based on functional annotation of		
RL	60,770 full-length cDNAs."		

DR EMBL: AK033873; BAC28503.1; --  
 DR MGD; MG1:97812; Ptpcd.  
 DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
 DR GO: GO:0006470; F:protein amino acid dephosphorylation; IEA.  
 DR InterPro: IPR003595; PTPC\_motif.  
 DR InterPro: IPR000387; TYR\_PP.  
 DR InterPro: IPR000242; TYR\_PP.  
 DR Pfam: PF00102; Y\_phosphatase\_1.  
 DR PRINTS: PR00700; PRTYPHPTASE.  
 DR SMART: SMO0404; PTPC\_motif.1.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE: PS50056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE: PS50055; TYR\_PHOSPHATASE\_PTP; 1.  
 DR NON\_TER  
 FT NON TER 1 1  
 SQ SEQUENCE 93 AA; 10642 MW; 1BCCF472432BA0CD CRC64;

Query Match 3.0%; Score 14; DB 11; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 394 VHCSAGVGRGVFI 407  
 |||||  
 Db 23 VHCSAGVGRGVFI 36

## RESULT 11

Q9UM23 PRELIMINARY; PRT; 134 AA.  
 AC Q9UM23;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE Protein tyrosine phosphatase RQ (Fragment).  
 PTP-RQ.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Dayton M.A., Blanchard K.L.;  
 RT "Differential expression of PTPase RNAs resulting from K562  
 RT differentiation induced by PMA."  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF169351; AAD50277.1; --  
 DR HSSP; P18052; IYFO.  
 DR GO: GO:0016787; F:hydrolase activity; IEA.  
 DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
 DR GO: GO:0006470; F:protein amino acid dephosphorylation; IEA.  
 DR InterPro: IPR000387; TYR\_phosphatase.  
 DR InterPro: IPR000242; TYR\_PP.  
 DR Pfam; PF00102; Y\_phosphatase\_1.  
 DR PRINTS; PR00700; PRTYPHPTASE.  
 DR SMART; SMO0194; PTPC; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 1.  
 KM HydroLase.  
 FT NON\_TER 1 1  
 FT NON\_TER 134 134  
 SQ SEQUENCE 134 AA; 15344 MW; 6EE48021FC54368C CRC64;

Query Match 3.0%; Score 14; DB 4; Length 134;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 394 VHCSAGVGRGVFI 407  
 |||||  
 Db 99 VHCSAGVGRGVFI 112

## RESULT 12

ID Q9Y1X3 PRELIMINARY; PRT; 183 AA.  
 AC Q9Y1X3;  
 DT 01-NOV-1999 (TRENBLrel. 12, Created)  
 DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE SPTPR3 (Fragment).  
 OS Ephydatia fluviatilis.  
 OC Eukaryota; Metazoa; Porifera; Demospongiae; Cernatinomorpha;  
 OC Haploclerida; Spongillidae; Ephydatia.  
 OX NCBI\_TaxID=31330;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=99246376; PubMed=10229569;  
 RA Ono K., Suga H., Iwabe N., Kuma K., Miyata T.;  
 RT "Multiple protein tyrosine phosphatases in sponges and explosive gene  
 RT duplication in the early evolution of animals before the parazoan-  
 RT eumetazoan split."  
 RL J. Mol. Evol. 48:654-662(1999).  
 DR EMBL; AB019128; BAA82561.1; --  
 DR HSSP; P18052; IYFO.  
 DR GO: GO:0016787; F:hydrolase activity; IEA.  
 DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
 DR GO: GO:0006470; F:protein amino acid dephosphorylation; IEA.  
 DR InterPro: IPR000387; TYR\_phosphatase.  
 DR Pfam; PF00102; Y\_phosphatase\_1.  
 DR PRINTS; PR00700; PRTYPHPTASE.  
 DR SMART; SMO0194; PTPC; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 1.  
 KM HydroLase.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 183 AA; 20507 MW; AEC07BFF661EDBEC CRC64;

Query Match 3.0%; Score 14; DB 5; Length 183;  
 Best Local Similarity 100.0%; Pred. No. 3e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 391 PLVHCSAGVGRG 404  
 |||||  
 Db 109 PLVHCSAGVGRG 122

RESULT 13

Q8C922 PRELIMINARY; PRT; 192 AA.  
 AC Q8C922;  
 DT 01-MAR-2003 (TRENBLrel. 23, Created)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Unknown EST (Fragment).  
 PTPRD.  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
 RX MEDLINE=2354683; PubMed=12466851;  
 RA The FANTOM Consortium.  
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK043201; BAC31488.1; --  
 DR MGD; MG1:97812; Ptpcd.  
 DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
 DR GO: GO:0006470; F:protein amino acid dephosphorylation; IEA.  
 DR InterPro: IPR003595; PTPC\_motif.  
 DR InterPro: IPR000387; TYR\_PP.  
 DR InterPro: IPR000242; TYR\_PP.

DR Pfam; PF00102; Y\_phosphatase; 1.  
 DR PRINTS; PR00700; PRTYPPHTRASE.  
 DR SMART; SM00194; PTPC; 1.  
 DR SMART; SM00404; PTPC motif; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
 DR NON\_TER  
 FT  
 SQ SEQUENCE 192 AA; 22551 MW; B78B194500F33B1A CRC64;

Query Match 3.0%; Score 14; DB 11; Length 192;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 394 VHCSAGVGRGVFI 407  
 DB 122 VHCSAGVGRGVFI 135

## RESULT 14

Q62917 PRELIMINARY; PRT; 460 AA.  
 AC Q62917;  
 DT 01-NOV-1996 (TrEMBLrel. 01; Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01; Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24; Last annotation update)  
 DE LAR receptor-linked tyrosine phosphatase.  
 OS Rattus norvegicus (Rat).  
 OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague Dawley; TISSUE=Brain;  
 RX MEDLINE=94073340; PubMed=8253779;  
 RA Longo F.M., Martignetti J.A., Le Beau J.M., Zhang J.S., Barnes J.P.,  
 RA Brosius J.;  
 RT "Leukocyte common antigen-related receptor-linked tyrosine  
 RT phosphatase. Regulation of mRNA expression.";  
 RL J. Biol. Chem. 268:26503-26511(1993).  
 DR EMBL; U00477; AAC04306.1; -.  
 DR PIR; A56493; A56493.  
 DR HSSP; P18052; LYPO.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0006470; F:protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR000387; TYR\_phosphatase.  
 DR InterPro; IPR000242; TYR\_PP.  
 DR Pfam; PF00102; Y\_phosphatase; 2.  
 DR PRINTS; PR00700; PRTYPPHTRASE.  
 DR SMART; SM00194; PTPC; 2.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Hydrolase; Receptor.  
 SQ SEQUENCE 460 AA; 52989 MW; B78C8B504F1260FA CRC64;

Query Match 3.0%; Score 14; DB 11; Length 460;  
 Best Local Similarity 100.0%; Pred. No. 7e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 394 VHCSAGVGRGVFI 407  
 DB 390 VHCSAGVGRGVFI 403

## RESULT 15

Q91BA5 PRELIMINARY; PRT; 468 AA.  
 AC Q91BA5;  
 DT 01-OCT-2000 (TrEMBLrel. 15; Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15; Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24; Last annotation update)  
 DE RPTPR2Aa protein (Fragment).  
 GN RPTPR2Aa.  
 OS Potamotrygon motoro (South American freshwater stingray).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Squales; Hymnosquales; Pristigaster; Batoidae;  
 OC Myliobatiformes; Myliobatoidae; Potamotrygonidae; Potamotrygon.  
 NCBI\_Taxid=86373;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20219325; PubMed=10754074;  
 RA Ogo-Koyanagi K., Suga H., Katoh K., Miyata T.;  
 RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:  
 RT divergence of tissue-specific isoform genes in the early evolution of  
 RT vertebrates.";  
 RT J. Mol. Evol. 50:302-311(2000).  
 DR EMBL; AB033581; BAA95188.1; -.  
 DR HSSP; P18052; LYPO.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
 DR GO; GO:0006470; F:protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR000387; TYR\_phosphatase.  
 DR Pfam; PF00102; Y\_phosphatase; 2.  
 DR PRINTS; PR00700; PRTYPPHTRASE.  
 DR SMART; SM00194; PTPC; 2.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Hydrolase.  
 FT NON\_TER  
 SQ SEQUENCE 468 AA; 53862 MW; 0051F5E0EDD7A580 CRC64;

Query Match 3.0%; Score 14; DB 13; Length 468;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 394 VHCSAGVGRGVFI 407  
 DB 398 VHCSAGVGRGVFI 411

Search completed: June 18, 2004, 19:48:43  
 Job time : 46 secs